

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCTGCTCGGTAGACCTGGTGCAACCAACCACTGGTTGGGTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGGGTTTTCCACCAGCTTTTACCAGGCCTCCCTCTGTGTGAAGAATTCATCAGCAAGAATCATATGGCTGTAAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA GAAGTGGCCAAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAATGATCAGATGGGAAGATGGTTTTTGTGCTGGAGGGGCTGCTGTTGGTCTTTGGAGCATTTGCTACTATGGCTTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGTATGTCAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACGCTTTGTCTGCCATAGCAATCAGCAGAACGCCTGTCTCATGAACCTCATGATGAGAGGCTCTTGGTGACAATTTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATACCATATGACCAGAGCCAGGCCAAAGCATCTTGCTTGGTTGTACATTTCTGGTGTGATGGGTGCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGATACAGCTGGCATTGTGGGAGGCCTCCACTGTGGCCATGTGTGGCCCACTGAAAAAGTTTCTGAACATGGGTGCAACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATGTTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATTAGTCTTTTTCAGCATGTTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAATGATCACCAGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGATACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAAAATGCAAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGCATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATATTTAAATGTTCCGGTAAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGTCAGTAATCCTCTCCCAAAATAAGCACACACATTTCAATTTCTCATGTTTGAAGTATTTTAAATGTTTGGTGAATGTGAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAAATTTAGTAGGTTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGTGCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACAGAGAGAAGGAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTAGTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCAATTTGTACATTCATTTGCTGAACCTTAACAAACATGTTTATCCTGAAACAGGCACAGGTGATGCATTCCTCTGCTGTTGCTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTTCATGTTTGAAGTTTGTACAGAAATGTTAATCATACAGAGAATCCTTGATGGAATATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAAATAACTTTAAACATATCTCAAGAGAAAATATCAAGCATGAATATGTGCTTTTCCAGAATCAACAGTATACTCATG

MLAARLVCLRTLPSRVFHPAFTKASPVVKNISITKNQWLLTPSREYATKTRIGIRRGRGTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAGVLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMMFMRRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLIGGLPLLRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
VGVLGLVVFVSSGLSMGFLPTTVAGATLSIRAWYGGGLVLFMSMFLLYDQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLTAGGNNRK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCCTCCGCTTCTGCAT
CGCGGCTTCGGCGGCTTCACCTAGACACCTAACAGTCGCGGAGCGCGCGGCTCGTGAGGG
GGTCGGCAGCGGGAGTCGGGCGGCTTGTGCATCTTGGCTACCTTGTGGGTCCGAA**ATG**TCGG
ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTTCGGCGCACCGCTC
GCCGTGGCCCTTGGTCGGCAAACTCGGCGCTCATCAGCCGCGCTACCTCTTCCCTCTGGCCGGA
AGCCTTCCTTTATCGCTTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTCTGGT
GTCCAGGAACCTGGATTCTTTATTGGTCAATTTATATTTCTTATCAGTATCTCAGCGGA
CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAAGCTG
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
TGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
ACACGATTTAAGGCCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAG
CTCGGTAATCAATGAGCTTTATGGAAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGGTACCGCTGG
CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATAGCGCGAGC
TGCTGATCAGAATGGCGGAGCGGGAGACACAACCTGGGGCCAGGGCTTTTCGACTGGAGACC
AG**TGA**AGGGGGCGGCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCTCCAGTGCTGGGTG
CACTTAACAACCTGCTTCTGGCTAACACTGTTGGACTTGGACACTGAACACACTGAATGTAGTCTTTC
AGTACGAGACAAGTTCTTAAATCCCCGAAGAAAAATATAAGTGTCCACAGATTTTCACGAT
TCTCATCTCAAGTCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAAACCTGAC
TACATTTTGGTGTCTTCTCTTCTCCCTTTTCCGCTCAATAATGGGTTTAGCGGGTCTCT
AATCTGCTGGCATTGAGCTGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT
TCTTGACACATGCCCTCTCTCCACTTTTCCCAACCCCACTTTGCACTAGAAAAAGTTG
CCCTAAAAATTTGCTGCTGCCCTTGACAGGTTCTGTATTATTATGACTTTTGCCAAAGCTGGTC
ACAACAATCATATTCAGCTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
AAGACAACCCAGGATGAAGCGTTTCTCAGCTTTTGAATTTGCTTCGACTGACATCCGTTGT
AACCCTTTGCCACTCTTCAGATATTTTTATAAAAAAAGTACCACTGAGTTCAIGAGGGCCA
CAGATTGGTTTATTAATGAGATACGAGGGTTGGTGTGGGTGTTTGTCTCAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
TTTGGCTTTCATATGATGCTACTGGCTTTGTGTAGCTGGGAGTAGTTGGTGGCTTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCTGGGCTTGT
ATTCCCAATTCACATCTCATTTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGCCCTATA
CGCTATTTAAATGTCACTTTTGGCTATCCCCGTTTTTTTGGTCACTGTTCAATTAATTTGT
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTGAAGATCATTTGGGTTTGGAGGTGTGTTA
TTTTTGAGTCAATAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACTTTTTT
TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAATAAGGTTTTTGAAGGCCA
TGGCTTTTTCACACAGTTATTTTATTTATGACGTTATCTGAAGCAGACTGTTAGGAGCAGT
ATTGAGTGGCTGTACACTTTTGGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
TTCAGGAACACTTGTGCTCTAACAGTATGACTATTTTCCCCCACTCTTAAACAGCTGTGAT
GTGTGTTATCCTAGGAAATGAGAGTTGGCAAAACACTCTCATTTTGAATAGAGTTTGTGTG
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTGGAACCTTAACTGTCA
TGTTTTGTGTTTCATCTGTGGCCACAATAAAGTTTACTGTAAATTTTACAGGCCATTA
CCAATTATGTGTGACGCTACACTCATTTGACAGGCGTGGAGCAGTATGATGTATAAGATA
TTTCTGACAGCTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACAGTCACTGCTGCTGGAG
CAGTCACTTTTTTCTTAAAGGTTTACAAGTATTAGAAGTTTACGTTACAGGCAAAATGTTC
ATGAAGTTATTTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT
ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGTGACTTGAACAGGCAAAACA
TGACAGTGGATTCTCTTTACAAATGGAATAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
TTTTTGTAACATAATCTTTTATTTGTTGTAATAATGTAATAATGTCACACTT

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FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSEFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGGERL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAGTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGCCCCAAAGCCCTAACCGGGGTCCGCGGCTCTGCGCTAGGGATCTTCCCCTGTGCC
 CCTTTGGGGCGGG**ATGG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGCGATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTGTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTCTCTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCAGTGAAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAAACAGAAGAAGCTTCGGCAACGAGAAGCACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEDEVWVESIAGFLRGPDSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQA ILQP
VLA AEDFTIFKAMMVQKN IEMQLQAIRIIQERNGVLPDCLTDGSDVVS DLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAATMNN SQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSE TSSLPQKGLKIPGLEHASIEGP IANLSVLGTEELRQREHYLKQKRD KLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRL LAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA



FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGAGTGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC
 AGTGGAAATGGAAAAACAGTGCCTGTAGTCATCTGTAATATGCTCCTTGTGCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTTCATTGCTTTAAGCTCAAGTCGATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCACTTCTGTGTTATAAAGAAAGATCATCAAAAGTAG
 AAAATTTGAAATATGCTTCTCGGAAGGAATTTCTGTATTTTCATGAAGTGGTCCATTCTCGCTT
 TTTCTTATTTCTCGGATAACTTGATTGCTTCTCATGTCTGTCTCTATCTTCAACGACCATG
 GCTGTATCTCTTCAAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAA
 GAGGCGCTTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTAGCCCTTCCAATTCTGTGCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAGAGCATCTTCATACA
 GAACAGCAAACTCATTTTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCTTCAGAGGA
 GATAACCGTGATCAGATTAGAAGCTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTTCCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTCTCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTACCAGTGTCAATTATCAACAAGTGTCTGTGCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTCACATTTTCAGTGTGTTGTAATATTATCTTTTCAGTTTGATA
 AACCAGAAATGTTTCAAATCCATAATTTCTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGTCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 CTTCCTTTTAACTTATAAAAAGCTAGGTTGTCTTTTGAATTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCTTTCTAAAAACGTTTGGTTGAAGGACCAATAATAC
 CTGGCCATACCATAGATTTTGGGATGATGTAGTCTGTGCTGCTAAATATTGCTGAAGAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTTAGAAATTCATGGGAAATTTGGATTTTTGT
 AATAATCTTTGATGTTTTAAACATTGTTCCCTAGTCAACATAGTTACCAGTCTGTATTTTA
 AGTCAATTAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAATATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAAATGCTGGCTTCAGAAATCATAC
 CAGATTGTGTCAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACCATGTTGACTTTTAACTGATGATGAATATTAATCTCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACCTTTACAGTGCTACTTCACACTTAAAGAGTGCATGGTATTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA
 AAATTAGCAAAACAAAGTGACTTGCTCAGGGTCATCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTGATGTTTACAGACTACCATACTGTAATATGAGCTTTATGGTGT
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAAGATGAATATA
 AGGTAATATACTATTATAAATTCATTGTGATATCCACAATAATATGACTGGCAAGAAATTG
 GTGGAAATTTGTAATTAATAATATTATAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPMAMV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPKRDNCATAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTGTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTC
TGGATAACTTGATTGTCTTCTATGTCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGATAGTGCTGAAGAGGCGTCTAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGCGGCGGCG
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCGCTGCGGGGCGAGGAGCAT
 CCCGCTCTACAGGTCCTCAAGCGGCGTGGCCGCGGGTCTATGGCCAAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCATGAACGCCCGGCCA
 GGTGAAGAAGAACCGAAAAAGAGAACAACAGTTGTCTGTTTGCACAAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGFGCCCTGGGTTTCTTCTTCAGATCTAC
 CTATTG**CATC**TGGGCTCAGGTGGGCCCCCTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGAAATCCCCCTGGACCTGCC
 TGGGTGCCTTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTATTGCCTACTTCTCT
 ATCTGGTTCGTGCCGACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCTCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACGCCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCCTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACTTCCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCAATTGTCTGTATCTATATAATCTG
 TGCTGTCTACCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCACGACGCTG
 AGCCAATCGCTACTTCCGGGCGCTACGGCTGGTCACTAGCCACGGCCATACATCAAACCT
 ATTTACTGGCTTGCCTTCACTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC
 TACCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTACCAGTTTGCCTCTGGAGTGTC
 ACTGGGCATTTCTACCCTCAGCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG
 CTGGGCGTGTCTCTTCAAATGTACCCCATTGATGAGGAGAGGCGGCGGCAGAAAGAA
 GGCCCTGCAGGCACTGAGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCT**CTAG**CGGCCCGCCAGTTGCCCGAAGCCACCATGCAGAAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGA
 CTGAAGACTCAAGGAGGTGCCCCAGGACACTGTCTGCTCACTGTGGGGCCGGCTGCTGTG
 TGGCTCCTGCTCCTCCCTCTGCTGCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACATAATGTAGAACCCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

MWLRWALS LPPSSCLWAE PGMPSQT PWWASAS ANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGTCF SIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGGQIVGQADTPCFQDFNSSTVASQS ANHTHGTTHSHRETQKAYLLAAGVIVCIYICAV
ILILGVREQREP YEAAQSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVADAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTSLSDFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRQNKKAL
QALRDEASSGCSGETDSTELASIL

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTACT
ACCCTGGTCCATGCTGCCATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATG
 GGTGGTTTCAGCAAGGCCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTATAAGCAAGTTCATGCTCTGAGTCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAAACAACCCTTTTGTGTCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGCTCTATGTCTATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAGAAGCCATTTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
 TTA AAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATTGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTACAGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLLFCEGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCCCVLTSGATCCYLLSS
 IFGKQLVVSYPFDKVALLRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALEFSWDTVFKLLAIAMVALIPGTLIKKSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCCTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCAC TGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTCT
 AGCATTTTTTGTGCCAGTACCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGTGCTTTCTGAGCGGTGCTTCCATTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTTCACTCACCTGCCATTTCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAAGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLGSAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFPV
FTHLFFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCGGTTCTTCGCCCGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

CCACGGCTCCGCCCCGCGTCCGGCTGAACCCCTCTCTTTGGAGTCAGCACTGATGAGG
CAGGTCGCCCATTTGCAGCTGCAGACGTGCGCGAGCTCGAGGCGCTGCTCCTGGCTGTGTG
CCTCTGGTGGCCAGCTTCCTAGACCGTGCCTATGACGCGCTGAGGCGTGCAGCTGAGCTGCC
CTCCTCTGCCACCCACCAATGGCAGGCCCACTCTTTTGAAGCATCTCAGGCTTTTTTGTGCCA
CACCCGAATGGCGCCACTTCATCGCAAAACAGGTACAGCCAAACCATGCTCCAGTTTCAAAATG
GACACGTAATGCTAAGAGCCAGCACTTATGTTCAAGTTTCTTGGAAATGCTGCTGATGACATGCT
TATGACGAGTGGGCGAGCGGCCAGTTGGGAGCGGCCAGAGATGCTGGGGCTTCCAGGAGG
TGGTGTGGAACTCTGCGCAGAGGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGGCTG
AAGCAGCAGGCAACGCGAGCACTCATGTGGCGCTGCTGCATCGGGGGGCGCTGTGGGCGCAGC
CGCCAGGCCCATGTGGGGCGCTGGGCGCTGAGGACAGCACTCCCATCCCGCTGGAAATGCTGCC
CGCGCGAGACATATTACCGATCGTCTGAAGCTGGTGGCCCAACATCACTTCGACCTCAAC
CTGGAAGCCAGCGCTCTCCGAGACATCTGGGTGAGGTTCCCTCGACACCAGGAGAGGCG
TCACTGCTCTGGGAGTGAACAAAGAGGCCAAAGTAGCAACCCCAACGAGTTGCTGCAAG
AGGACAGCTCGGCCGAGGACAGAGCTGGTGACAGCTGGAGACCCGATGGAGCGAGCAAGACTG
GATGACGAGCTGAGAAGCTGGTGTCTCGGCCGAGTGCAGCTGGTGAAGGTAAGTGGCGT
GGTCCGAGGGCTCTGAGAGTCAACCAACAGAAATGTATCACTTACAGATGGCAGCACTGAGC
CGTGGAAACCGAGGAGGGCATGGCTATGATTTTCGGCGGCCCACTGGCCAGCTGCGTGAG
GTCCACCTTCGGCGCGTTTCAACCTGGCGCTTTCAGCACTTGAAGCTCTCTTTATCGATCAGGC
CAACTACTTCTCAACTTCCCATGCAAGGTGGGCGAGCCAGCCAGTCTCATCTCTAGGCAGA
CTCCGAGACCCCAAGCTGGCCCGCTCCCAACCCCATACCCAGGTACCGAACCAGGTTGATCTCG
TGGCTCTGGCGCTCAGGCCCGCTTCAAGGTACTTAAGCAGCTGCGCTCCCCAGGAGAT
GCTGCGTCTCAAGGCTTACCCAGAAATGGGTACAGCTGAGATATCTCAACTTCGAGTACT
TGATGCACTCAACACCATTCGGGGCGGAGCACTACAATGACCTGTCTCAGTACCTGTGTTC
CCCTGGGTCTCTCAGGACTACGTGTCCCAACCTCGGACCTCAGCAACCCAGGCTCTTCCG
GGACCTGTCTAAGCCCATCGTGTGGTGAACCCAAAGATCGCCAGCTCGTGGGGAGAAGT
ATGAAGAGTTTGGAGGACCCAGCAGGGACATTAACAAGTTCACTATGGCACCCACTACTCC
AATGACGAGCGGTGTGATGACTACTCTACCTCTCGCGTGGAGCCTTCACTCTCGTGCAGTCCA
GTGTCAAAGTGGCCGCTTGAAGCTCTCCGACCGGCAAGTTCCACTCGGTGGCGGACGCTGG
GGCCAGCGCTGAGAGCCCTCCGATGTGAAGAGCTCATCCCGAAATTTCTTCACTTTCTC
GACTTCTCGGAGAACCAAGACGGTTTGTGACTGGGCTGTCCAGCTGACCAACGAGAAGT
AGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCTGAGGACTTCATCAGCAGACCGCC
AGGCTCTGGAGTGGAGTATGTGCTGCACACTACACGAGTGGATGACTACTCATCTTTTGG
TACAAGCAGCGGGGCGAGCCGCGAGGAGGCCCTCAATGCTCTTATTAATCCACTATGTA
GGGGGCTGTAGACTTGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
TCAGCAACTTGGGCAAGCTCTCTGTACGTCTGAAGGAGCACTTCAACTCGGCTCTCA
CTTGAGGAAAGCAGCCCATCGCTTGCACCTGGACACTAACTCACTAGCATCTTCCAGCA
CTTGAGCAACTCAAGGCATTTCTTCGAGAGGTGACTGTGATGCAATGGGCTGCTGGGCA
CCACAGCTGGTTGCCCTATGACGCAACATAAGCAACTACTTCAGCTCAGCAAAAGACCC
ACCATGGGCAACCAAGACGAGCACTGCTGATGTGCCCTGGGTGGCAGGCAAGTGTGTG
GAGTGGCAACAGCACTGCGAGTGGCCCGGATGAAGAGCTGCTATTCAGCGCTGGCCACTGG
ATGCGAGGCTCGGGGTGACTGCATACCCCGTGCAAGCTGTTGAGCAGTGCAGCTGCCAC
CTTGATGTAGTAACTGCTTGTGCATGGACACTGTGGCATCTACTCATCTCAGGCTCCG
GGACCAACCACTGTGATGTGTGGCGCTCTGCATCAGGTGGTGTCTGTCACTAGGCGTGGC
CAAGCTCTGTGCAAGTCTGTGATGGGCATGGGGCTGCAGTGATCTGTGCGCATTCAGACCT
CTGATGACATGGCTGTGCTGTGATCTGAGGATGGAAGTGTGATCATACCACTGACGCG
CGGACAGTTTGTAGCGGACCACTCGGCTCTGGGTGGCCACATTTCCCTGGACCTATTTTCCACC
TGGCATTTGGGTTCGGAAGGCAGATTGTGGTACAGACTCAGCGTGGGAAGCTCTCGGGCG
CAGGTCACTACTCTTTGCACTCTGATTCACTCAATGGGAAGTTGCGGGCTTCACTGCGCCCT
GGCAGACAGCCTCAGCGCTGACGGGTGACAGAGCAATTTGTTGTTCTGGGCAAGCCGCCAGT
CGCCGCTGCACATCTTCAACTAAACCACTGTCTCGCGGCCGCTCTCTTGGCCATGAAG
TGGCCATTCGCGAGCTGGGCGTGCACCAAGGAGCGACGACAGTGTGTTGGGCTGGAGGA
TGGCAAGCTCATCTGTGGTGTGCGGGGCGAGCCCTCTGAGTGTGCGCAGCAGCCAGTCTGCGC
GGAGCTGTGGGGCTCTCGCGGCCATCTCCGAGTTGCTCTGGGAGAGCAGGAATACAAC
CTTACTGAGGCGCGCTCAAGCACTGGCCAGTCCGCTGCTCGGGCGCCCGCCCGCGGACGGCTC
GCCCGGAAGGCCCGCCGGAAGTGGCGGGAACACCCGGGTGGGACGCCAGCGGGGTGA
CGGGGCGCCACCTGCGCCAGTCAAGGATTTGGCGGGCGATGTTACCCCTCAGGAGATTGGC
GGCGGAAGTGGCGCCCTCGCGGCTGAGGGCGGCCCTGAGGGCGAGCACTGGCGTCTC

FIGURE 23

MSQFEMDITYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAIEETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGILLEVTQNVFYFDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFYEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGLCLQLTNEKVGDDVLPWPASSPEDFIQQRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHLLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTDETVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGGKLI VVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGCTCTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTATGGGGTCTGGGGCTCTTC
 TGGACCCCTTAAGTGGGTACTTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCCTTTGCCCTCTT
 CTACTGGGCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACTGCGGTATTGGCATTGGAGCCCTCATCTGACCCCTTGTGCAG
 ATAGCCCGGGTCATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCTGCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTCGACAAAGTACAGA
 CCTGCTGTGTTCTTTGGGAAGCTGCTGGTGGTTCGGAGGCGTGGGGTCTCTGTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTTATGTATCGCCAGCGGCTTCTTCAGCGT
 TTTGCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACTGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACCTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKK
EAPPDNKKRKK

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**CTTCGTGCTCCGATTTCGCAAGAGTTCTACAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTC
 CAGTGTGACCCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTGCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCGGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGACAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGTCTTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAGGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAATCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCTTTCCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTGCAAAAGAACCGGCGCTGCAAAGTCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAAGCTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACCTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAATAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQLETA
LEHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVFPAYEDIFRDEEEDEEHSGNDS DGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGLQRH
VSRHNRHNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMD ISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGATACCAATTTTTCATGGAAAC
CAGCAAGGAGCGATACAGAAAAACCCCTCAACCACCAGGAGATAGACTACAGCCCGTAAATG
GCTGACTTTTGGCTATAGAAAAAAGGAAGACGAAAGAGACAGTCTTTTGTGGAAAGCTAA
GCTTCTCCCTTTATTCGAGTCAAGAAACCCGCCCTCTTGAGCTATTCACAGTTTAAACAATT
GAGTAAAGTAGCTCCGGTACCA**ATG**TGACAGCGCCCTGGGTCCCTCTG66CAGCGCTC
CTGCTCTTTCTCTGATGTGTGATATCCGTATATGTGGAGCTACCTTTGACAGAGCTGTG6C
CAGCGGCTGCCAACGGTGTCTGTGACTCTGAGGACCCCTGGATCTGGC CATGTATCTCAG
CCTCTTCTCTCGGCCGCCGCCACGCCCTCGCTGAGATCAGACCTCATATTAATACCATC
CTGAAGGTTGCAAAAGGGGACCCAGGCCCAATGGCGTTCGACGGGTACATGGCAGGGAGG
TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAGGGGTGCAAGGGGGAGATGGCAGGCCCT
GGCCCGCTGTGCCAGAGCGCTTCTTCCGCTTCTCAGTGGGCGCAAGTGGGCGCTGCCACGC
GGCGAGGACTTCACAGCGCTGCTCTCTGAAGAGGCTCTTGTGAATTTGCTGGGTTTGTGA
CATGGCGACCGGGCAGTTTGTCTGCTCCCTGGGTGGCATCTACTCTTACAGCTCAATGTGC
ACAGCTGGAAATACAAGAGACATCGTGCACATATGTCATACAGAAAGAGGCTGTGCATC
CTGTACGGCAGCGCCAGCGAGCGCAGCATCATGAGAGCCAGAGTGGATGCTGGACGCTGGC
CTACGGGAGCCGGCTGTGGTGGCGCTCTTCAAGCGCCACAGCGCAGAAAGGCATCTACAGCA
ACGACTCTGACACCTACATCACTCTCAGCGGCCACTCATAGGCCGAGGACAGC**ATGA**GG
CTCTGGGGCCACCTCCGGGCTGGAGAGCTCAGGTGTCTGGTCCCGCTGCCAGGCTCAG
TTTGCACTGTCTGTAAGAGGAAGGAGCGAGGAGTCCCGGGGAGCTGGGATCTGGGGAGA
CCCTGCTCTTATCTTGGCTGCCATCACTCCCTCCAGCTATTCTGGCTCTCTCTCTCTCT
TGGACCTATTTTAAAGAACTTGTCTACCTAAATATTCTAGAATCTTCCAGCGCTCAGTGGCC
AGCACTCTCAAACCTTGAAATGTCATGGGAATCAGTCGGGGCTTGGTGTAAATGCGATTTCT
GACTCAGCAGTCTGATGTGGGTTCAGGATTTCTGTCTTTATATGTTCTGGGTATGTCTG
ATGGGGTCAGTCTATGAACACATCGGAGCAACAGTTCTTACAGACTTTTCAAGTATCTAG
TACTTTCTCAACATTTCTGGAATCTCCCGCATTCAGAAATCTTCCCAACATTTTTTTTCT
TGAGACAGAGCTCTGCTCTGTTGTGGTGGTGGAGTGGAGTGTGCAATCTCAGTTCACTGC
AACCCTCGCTCCCGGGTTAAGCAATTTTCTCTCAGCCCTCCCTAGTGGCTGGGATATC
AGGGCGCTCTACAGAGCTGGTGAATTTTGTATTTTGTAGATAGTGGGTCTTCAACATA
TTGGCGAGGCTGTGTTGAATCTCTCACTCAGTGCACCCCGCTCGGCTCTCAAAT
GCTGGGATACAGTGTGGAGCAGCTGCTTCTCTTACCCCTTCCCTCTCTCTTGTCTCAGGC
CCCTCAGGCGCTCTGCTGCTATTTTCTCTTACCCCTTCCCTCTCTCTTGTCTCAGGC
TGCCACCTCTCACACACGCTTCAATTTATCTTAAACATGAACACTCACTCTGTGCTGT
CTCTGCGGAGGCTGAGGCGCTCAGACAGAGCCCTGCCCTCCCTCAGTCACTGGCCAT
CTCAGCGCGGGGAGAGATGTGTACATAGTTTAAAGACAGACCAGAGCTCATGGGG
GCTCTGTTCTTGGGTGTTCAAGTGCTGCTGTCTCTCAATTAACCACTGCTCCCAAGGCTGG
TGGAGCGGGTCCCGGTGGCAGGCGAGTATCTCCTTCCGTTCTCTATCAGCTGCCAG
TGCTCATCTGTTACAGCAAAACCCAGGCGGCTTGCCACAGAGGTTCTGTTGAGGAGAGG
ACCCAGGAGTCTGGGGCTTTGGGGGTGAAGTGGCCCCGAAGATGGAACCAACCAACCA
TAGCTCTCCCACTGCTATACGCTATCTCGGAGAAAGACTGCCCTCTCACTGGGATGCCA
CTTCTCGCTCTCTCCAGGCTCTGCCAGGCGCTGTAGTCCCTTCCCAAAAGTCACTC
GAACTCCGTTTCCCCAGGCGCTCCAGTGCCTCAGACATGATGTCTGTCGCCAGGTGCT
CTCTGCCCTCATGCCCTCTCAGCGGCCAGTGCCCGACTCTCAGGCTTTATCAAGGTG
CTAAGGCGCGGGTGGGACGCTCTGCTCTCAGAGCCCTCTCGGCCCTGGTGGCTGCTTTAC
AAACACCTGCAGGAGAAGGCGACGGAAGCCAGGCTTTAGAGCCCTCAGCAGGTTCTGGG
AGCTAGAGCAAAAGGAGGACCTCAGGCTCTCCGTTCTCTTCCAGGTTGGGTTGGCTGGT
GTTCCTCTAGCTTTCCAAACCCAGGTGGCTTGCCCTCTCCCAAGAGGAGGCGCGCTCGC
CCATTTGGTGTCTATGACACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTGTGTGCTCAC
AGCCGAGGGAGCGCTGGCTTCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCAGGA
AGCACTGTGCTATAAACCACTGCCGTGATCTCGCCCTGCTCAGCCCGCCAGCGCTGCC
GTCCAGCATGATTAAGAATGCTGCTCTCTCTTGAAAAAAGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
 ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPQGSKGDKGEMGSPGAPCQKRF
 FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
 YVHIMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
 FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGACCCGCCAGGAAAGACTG
 AGGCCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCGCGCGCGCCTCCCGGGACAGAAAG**ATG**TG
 CTCACGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTTGCATGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTAC
 AGAACCATGATCGCCAGCCTGCCAGCGGGGTCTTCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACC AATGAGACCTTCCGTGGCCTGCGCGCCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCTGGTGCCCTCGACACGC
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCTGGAGCCCGCAT
 CCTGGACACTGCCAACGTGGAGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACCGCCTGCGGCTGGCCGGCAACAC
 CCGCATTTGCCAGCTGCGGCTCCAGGACCTGGCCGGCTGGCTTCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCTGGGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTAGCCCTGAGCTGGTTTGCGCCCTG
 GGTGCGCGAGAGCCAGCTCACACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCGCCCA
 AGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCACTTTGGCTGGCCAGCCACACACC
 ACCACGCCACAGTGGCCCAACACGAGGCCCTGGTGCGGGAGCCCAACAGCTGTCTTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGACATGCCACCTGGGGACACGGCACCACTGGCGTGTCTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCACTCA
 CGCCGAGGCCACACGGTCCCTGACCCTGGGCATCGAGCGGTGAGCCCACTCCTCGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCTGATAAGCGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACAGGTCACCCAGCTGCGGCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG
 CCCGGGCGGGTGCCGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCCAAGCCGTCCA
 CTCAACACGCCCCAGTCAACCCAGGCCCGCGAGGGCAACCTGCGCTCCTCATTGCGCCCG
 CCTTGCCCGCGGTGCTCTGCGCCGCGCTGGCTGCGGTGGGGGACGCCACTGTGTGCGGGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAGGCCAGGTGGGGCGAGGGCTGGGCCCT
 GGAAGTGGAGGAGTGAAGGTCCCTTGGAGCCAGGCCAAGGCCAACAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGCTTCCAGGGCCTGGCCTC
 CAGTCAACCTCCACGCAAGCCCTACATCTAAAGCAGAGAGAGACAGGGCAGCTGGGGCGG
 GGCTCGCCAGTGAAGTGGCCAGCCCTCCTGCTGCCACACACAGTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
 CCTCGGCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCGAAGAC
 CGAGTGCTATGAGGACAGTTCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCGAGCGG
 GGCCCTGGCATGTGCTGGTAACGATGCTGGGTCTGCTGGGCTCTCCCATCTCAGGCGGA
 CCTTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGTAGGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCTGT
 GGAAGATGTTTTTCAACTCAGAGACAAGGACTTTGGTTTTGTAAAGACAACAGTATATG
 AAGGCCCTTTTGAAGAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPFDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQGAFTDLDRLLEKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRRLRAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFG
PWVRESHVTLASPEETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPQPDCCPPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQGTTPSPPTVTPRPPRSLTLGIEPVSPSTLRVGLQRYLQGSSVQLRSLRL
TYRNLSPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVAAVCVRRGRAMAAAAQDKGQVGPAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFFGPGQLQSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGGTTTTGAGCTCAT
 CTTTCATCTTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAATGAGACTCATCAG
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGTTGATGCTCCAGAGCTGCCAG
 AAGAAGGGGAAGCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACGCACACGCACTGGATTTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTCATCTCTGCTCCAAACTGAGAGTTTGTATCTATGCCATTAACAGAAATTCACAGCTGG
 ATCTCAAAACCTTTGAAATTCACAAGGAGTTAAGATATTAGATTGTCTAATAACAGACTG
 AAGAGTGTAACTTTGGTATTACTGGCAGGTTCTCAGGTATTAGATCTTCTTTTAAAGTACTT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAGAACTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCT
 TTCTTAGGATTTCAGAACTCTTCCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
 AAAACTGCACATTGTTTACCAATGGACACAATTTCTGGGTTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAATATTAGAATGACAATATAGATGGCAAAAGCCAAATTTGAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACCTCTGGGACACCTTTTCTTATCTTACAATTTGTTGGCATACATCAGTGGAACTAT
 TTCAGATCCGAAATGTGACTTTTGGTGTAAGGCTTATCTTGACCACAATTCATTTTGACTAC
 TCAAAATCTGTAATGAGAACTATAAAATGGACATGTACATTTCCAGAGTGTTTTACATTCA
 ACAGGATAAAAATCTATTGCTTTTGACCAAAATGGACATAGAAGAACTGACAATCTCAAGT
 CACAAATGTCACACATGCTTTTCCGAATTATCCTACGAATTCCTAATTTTAAATTTTGGCC
 AATAATATCTTAAACAGCAGGTTGTTTAAAGAACTATCCAATCGCCTCACTTGAAGAACTCT
 CATTTTGAATGGCAATTAACCTGGAGCACTTTCTTTAGTAAGTTGCTTTGCTAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAAATGATGAATAATTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTATACAATAAATGTCTGATTCTGTCTTCAG
 GTGCTTGCCCAAAAGTATTCAAACTACTGACCTAAATAATAACCAATCCAAACTGTACCTA
 AGAGACTAATCTATCTGATGGCCCTTACGAGAACATAAATATGCTTTAAATTTCTAACTGAT
 CTCCTGGATGAGTCAATTTTCAGTAGACTTTTCAGTTCTGAACATTGAAATGAACTTCAATCT
 CAGCCCATCTCTGACTTTTGGTTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCCGGAAGAA
 ATCCATCTCGGTGTACTCTGGAATTAAGAAATTTTCATTACAGTTTGAACATATTTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACATAG
 GTTAAAGAGCTTCACTCTCCACGAATTTATCTTGCAACACAGCTCTGTTGATTGTCACCATTG
 TGGTATTATGCTAGTCTCGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGGTTAGGAAAACAACCCCA
 AGAACCACTCAAGAGAAATGTCCGATTCCACGCATTTATTTTATACAGTGAACATGATTCTC
 TGTGGGTGAAGAATGAATGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGAATTTGC
 CTTTATGAAGCTACTTTGACCCTGGCAAAAGCAATAGTGAATAATTTGAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTCCTACTTTGCCCAACACAATCTCTTCCATGAAAATTTGATCATATAATTTCTATC
 TTACTGGAAACCCATTCCATTTCTATTGCAATCCCACAGGTATCATAACTGAAGCTCTCCT
 GGAAAAAAGCATACTTGAATGGCCCAAGGATAGGCGTTAATGTGGGGCTTTCTGGGGCAA
 ACCCTCGAGCTGCTATTAATGTTAATGTATTAGCCACAGAGAATGTATGAACGTGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTGTCT
ATAAATCCCAACAGTCTTGGGAAGTTGGGGACCACATACACTGTGGGATGTACATTGATA
CAACCTTTATGTTGGCAATTTGACAAATTTTATAAATAAATAATGGTTATTCCCTCATATA
TCAGTTCTTGAAGAGTTTCTAAGAAATGATCCTATAGAAACACCTTCACAAGTTTATGAAG
GCTTATGGAAAAAGGTTTCAATCCAGGATTGTTTATAATCATGAAAAATGTGGCCAGGTGC
AGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACAGGTTCAA
GAGATTGGAGACCATCTGGGCCAATGGTGAAACCTGTCTCTACTAAAAATACAAAAATTA
GCTGGGCGTGTAGTGTGCAGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGATTCG
CTTGAACCCGGGAGGTGGCAGTTGCAGTGGAGTGGAGTCGAGCACTGCACCTCAGCCTGGT
GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGGAAAAATCC
TCATGGCCACAATAAAGTTCTAATTCATAAATATAGTACATTAATGTAATATAATATA
CATGCCACTAAAAAGAAATAGGTTAGCTGTATATTTCTGGTATGGAAAAAACAATATAAT
GTTATAAATCTTAGGTTGGTGCAAACTAATTTGTGGTTTTGGCATTGAATGGCATTTGAA
ATAAAGGTGTAAAGAAATCTATACAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA
TACAGGAGCAATTTGATTCTATGTTGTGTATTCTATAATGTTGAATGTTTAGAATGA
ATCTGTATTTCTTTTATAAGTAGAAAAAATAAGATAGTTTTTACAGCTT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGRLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLLQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHDLsqNLLQHKNdENCsWPETVvNMNLSYNKLS
DSVFRCLPKSIQILDlnnnQIQTVPKETiHLMALRElnIAFNfLTDLPGCSHfSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNfiQLEtYSEVMmVGWSDSYtCEYPLN
LRGTRLKDVHLHELSCNTALLIVtIVVIMLVlGLAVAFcCLHfDLPWYLRMLGQCTQTWHRV
RKTTQEQlKRNVRfHAFISYSEHDSLwVKNELIPNLEKEDGSILIClyESYFDPGKSISENI
VSfIEKSYKSIfVLSPNfVQNEwCHYEFYfAHhNLFHENSdHIILlLEPIPIFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINvNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

[illegible]

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEWEERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNFPDLNLTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRRQRG

CTAAGAGGACAAGATGAGGCCCGGCGCTTCATTTCTCTAGCCCTTCTGTTCTTCTCTTGCCCAAGCTGTCAGGGGG
ATTTTGGGGGATGTGGGACCTCAAAATTCGACCGCGGGCTTCAGCTCTTTCCAGAGGTGTGACTCCAGCTCCAGC
TTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCGCAGCTTAGGCAGGGAGTGTCTGTGCCAGTTGT
TTCCAAATTTCCAGCGGCTCGTGAGGTACCCCTGGGACCTCCGAGTGGCTTTTCCCTCGGCAGACACACCTTT
CCGTGCGACAGATGGAACTGTTGAAATCACAGCTCATGTTCTTTCTCAGAAGTTTGAAGAAAGCAATTTCAA
GTGAGGGAATATGTTCCAAATTAATTAGTGTGATTAAGAAAGCAATGTAAACCTTAAGCTTCGGAATGCATCAT
GGAGAAGATACCAATTTTACACTGAAGCTGGAATCTCGAGTGAATGACAGTAGAAGTGAAGGAGATGAAAAA
TGCTCATCAGCTGAAGGAGAGTTTGTGGGAAGCTCAGAAATGTGCACCGCTGGAGGTGGAGATGAAGAAT
ATGACTCTTCTGGTAGAAGACTTGAGACACTAGACAAAACAATGTCTGCCATTCCGGCAGGAATCGTGGC
TCTCAAGACCAAGTGAAGAAGTGTGAGGCTCTAAAGATCAAAACCCCTGTGCTGCACCACTCTCTCCACTC
CAGGGAGCTGTGCTCATGTGTGTGTGAATCATGCAACCAAGCTGTGTTGGTTCAGCTCACTGGAGAGGGTTT
TCTTATCTATATGTTGCTTGGGTAGGAGTACTCTCCCGACATCAAAACAAGGACTATGTTGGGTGGCGCC
ATTGAATACAGATGGGAGAGCTGTGGAGATTAACTGCCACCAACCACTGGATGATTGCTATTTGATATAA
ATGCTCGAGAGTTGCGGATCACCTATGCGCAAGGTAGTGGTACAGCAGTTTACAACAACAACCTTACGTCAAC
ATGTGACAACCCGGGAATTTCCGAGAGTTAACTGACCAACCAACAGGATTCGTGACTCAAACTCCCTTAA
TGCTGCTATAATAACGCTTTTTCATGTCTATGCTTCTGGCAAGATTTGCACTTTGCTGTGGATCAGAATG
GATTTGGGTATTATTTCAACTGAAGCCGACGCTAGCTAAACATGGTATAGTAATCAATGACACCAACT
CAGGCTGAAACACTTGGTATACCAAGCATATAAACCTCTGCTTTCAACGCTTCATGGTATGTGGGTTCT
GTATGCCACCGGCTACTATGAACACAGAACAGAGAGATTTTACTATTGACACAACACAGGGAAGAGG
CAAACTCAGAGCTTGTAAATCGATATAGTGCAGGAAGAAAGTCAGAGCACTTAACTTAAOCCCTTTGACCAAAA
CTTTATGCTATAACGATGTGTACCTTCTGAAATATGATCTTTCTGTCTGCGAAGGCCCGCAGTCAAGCTGTTA
GGATTTAGGGTGAAGAGAAAAATTTTGTGAAAAATAGTCTTCTCCACTATTAGATATTCTCGAGGGTGT
CTAAAGTGTGTTTCATTTTGCAGCAATGTTTAGGTGATCAGTTCTACCAACTAGAGATTAGGACATTTGTCT
TGATTTTGCTGATCTTCTGGGAATCATCTGCCCTTTCAAGGCCATTTTGAATTAAGTCTGTCTAGGGTGGGA
TTGTACAGACTCTAGGGGCCACTCTGGGCTAGTGAAGGCTACTGTGAGGGGCTCAGTGAAGACCTTAAATTA
GGAATTAAGCAATTAATAACTCAGTATGGCTGTAGGATTCCTTTGACAGGAATATTGCCCAATGCAATGCT
CTCATCTCATGTAGCCACCACTAAATCTTCCATGCTCGGCAAGAACTGGGCACTTAGTTAGGTAGATTAATAT
GGAGCTCTCTCGAGGAGCAAAATCTCAACTTTTTTTTCCGCTCACTAGCACTGGAAATGATGCTTTGTATGGC
CAGATAAGTAATTTGGCATGCTTATATATTCTACACTGTAAAGTGTGAGTTGTCTGGAGAGAGGCCCTTTT
ATGCAATTAATTTACATAGCAAAATTAATCCAGAAGGATCTGTAGTGAAGGACCTGTGCTTTCTTCTCT
ATTGTCCACTCTATAAAGTCAGTAGAATCTCTACCTCAACTCTCTTCAAAGCAGCTCAGAAGATTAG
AACCAGACTCTATACCAATTTCAACCCCCAACCCCTCTCTACTGCCCTATTAATAAGTTTCTTCT
CTATGGAACCTGATCTAAGATTTGAAAAATTAATTTTCTTAATTCATTAGGCACTTTATTACATGACTCTA
AGACTATAAGAAATCTGTAGTCAGTGTGCAAAAGTGTAGCATTAATGTGATCTATAAAGACCTTTGAGCATA
TGTGCAACTTTTAGTGATGTACGACTGTGTGCAATGTAATTTTGTCTTTTGAAGCTGGAACCTTGAAAAAT
GAAATTTAAATTTTCTTTCTAGGAGAGGATTTGAAAAAGCAATTAGGAGATCTAGTTAATCTAGCTGCAGTAGT
TGGAAACCTCTGCTGGTGTATGATGTCTCTGTGCTTTTGAATGACTTATCATCAATGCTCTTGTCTATT
TCTTTGTGATGTCAAGTCTTAGTTCTATAGGATGTGCGATTTAAATGCTTTACTCCCCCTTTAAATTAATGAT
TAAATGTGCTTTTAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSFFFFSSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGlyWVAPLNTDGRLLLEYRlyNTLD
DLLLLYNARELRITYGQSGTAVYNNNNMYVNNMYNTGNiARVNLTNTIAVTQTLpNAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCVGLYATRMTNTRTEEIFFFFYDTNTGKEGKLdivMHKMQEKVQSINYNPFdqKLYVNDG
YLLNYDLSVLQKPQ

0000172.11501

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCCATTGAATACAGATGGGAGACTCTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCAGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCAC TTTTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAAC TTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTTGNTATGCCGATGCTGTCTTAGTGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAAC TGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGITTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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1
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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTTCGGCGCCGGCGCGGCTCTCCAAT
 GGCAAATGTGTGGCTGGAGCGAGCGCGAGGCTTTCGGCAAGGCAGTGCAGTGTTCGACAGCCGGGGCAGG
 TCCTGTGGAAGCAGATAAAAGAAAACATTTATTAACTGTCTATTACGAGGGGAGCGCCGGCGGGGCTCTCCG
 ACTCCCGCGCGAAGATTTGGCTCCCTCCAGTCCGAGAGAGGAGAGAAGAAAGCGGAAAGAGGCAGATTAC
 GTCGTTTCCAGCCAAATGGACCTGATCGATTGGCCCTCTGAATTTATCAGATATTTGATTTATTAGCGATGCC
 CCCTGGTTTGTGCTGTACGCACACACCTGCACACAGGCTCTGGCTCGCTCCCTCCCTGTTTCCAGCTCC
 TGGCGAATTCGCACATCTGTTTCACTCTCCGCGAGGGCGAGCAGAGCAGATGTCTCGAATCTGCGAGTGG
 AAGAGGGCAGGGGAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAGAACACCCAGAT
 CAGCAAAAAAAGAAAGATGGGCCCGCCGAGCTCTGCTGTGCTTTCGGCAACTGTGTTCTCTCTGCTGGG
 TGGAACTCGGCTTCTGTCTGCACACCCGCTGAAAGGCAAGCTTTCAGAGGGACCGCAGGAACATCCGCCCA
 ACATCATCTCGTGTGACGGACGACAGGATGTGGAGCTGGGTTCATGCGAGTGATGAACAAAGACCGCCGCG
 ATCATGGAGCAGGGCGGGGGCGCATTTATCAACGCTTCTGTGCCACACCCATGTGCTGCCCTCCAGCTCTCT
 CATCTCTACTGGCAAGTACGTCACAAACCACACACTTACACCAACATGAGAAGTGTCTCTCGCCCTCTGCG
 AGGCACAGCAGGAGAGCGCACCTTTGCCGTGTACTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACAACGGCTCTTACTGTCCACCCGGCTGGAAGGAGTGGTCGGACTCCTTAAAAACTCCCG
 CTTTATAACTACACGCTGTGTCCGAGCGGGGTGAAAGAGAAGCAGCGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATCCCAATGACAGCGCTGAGCTTCTTCGCACTCCAAAGAGATTACCCGACAGGCCAGCTCTCT
 ATGGTCTCAGCGATTGACGCGCCACCGCCCTGAGGATTCAGCCCCACAATATTACGCTCTTCCCAACCG
 ATCTCAGCAGCTCAGCGGAGCTACAACCTACGCGCCCAACCCGAGCAACACTGGATCATGCGCTACACGGGG
 CCATGAAGCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGTTTGACAGCCCTCATCTCGGTGAAG
 GACTCATGGAGAGGATTACAACTGCTGGTTGAGACGGCGGAGCTGGACAACACGATACATCTGATACACCGC
 CGACCCAGCTTACCACATCGCCAGTTTGGCTTGGTGAAGGGAATCCATGCATATGATGTGATCAGAGG
 TCCGCTTGTACTGTAGGGGGCCCAACGCTGGAAGCGGCTGTCTGAATCCCCACTGCTCTCAACATGACCTG
 GCCCCACCATCTTGGACATTCGAGGCTGGACATACCTGCGGATATGGACGGGAATCCATCTTCAAGTCTG
 GGACAGGGAGCGGCGGTGAATCGGTTTCACTTGAAGAAAGATGAGGGTCTGGCGGGACTCCTTCTTGGTGG
 CAGCGTGGAAGACCTGTCTCAGCTGCTGAGTACAGACGGCGTGTGAGCAGCTGGGACAGAAATGGCAGTG
 TGTGGAGCGCCACCGGGGAAGCTGAAGCTGCTAAGTGCAAGGGGCCCATCGCTGGCGCGGACGAGAGGCC
 TCTCCAACTCTGCTCCCAAGTACTACGGCGAGGGCAGCGAGGCTGCACTGTGACAGCGGGGACTACAGCTC
 AGCTGGCGCGGACCGGGAATAACTTTCAAGAAGAAGTACAAGGCGCACTGTGTCCGCACTGCTCTCCATCCG
 CTCAGTGGCCATCGAGGTGAGCGGCGAGGTGTACCACTAGGCTCGGTGTGTCGCCCGAGCCCGCAAACTCA
 CCAAGCGCACTTGGCCAGGCGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGAGGCG
 TCTCCGACTACTCTAGCGCCCAACCCATTAAATGACACATCGGTGCTACTCTAGAGAACGACACATCCA
 GTGTGACTTGGACCTGTACAAGTCCCTGAGGCGCTGGAAGACCAAGCTGCACATCGACACAGAGATTGAAC
 CCTGTGAAACAAAATTAAGAACCTGAGGGAGTCCGAGGTCACTTGAGAAAAAGCGGCGAGAGAATGTGAC
 GTGCACAAAATCAGTACCACACCCAGCAAAAGCGCGCTCTCAAGCAGAGGCTCTCAGTCTGCTACTCTTTCAG
 GAGGGCGCTGCAAGAGAGAGACAGGTGTGGCTGTTGGGGAGCAGAAAGCAGAAAGAACTCCGCAAGCTGCG
 TCAAGCGCTCGAGAACAGCAGCGTGCAGCATGCAAGGCTCAAGCTGCTTCCACCCAGCAGAACCGACCTGG
 CAGCGCGCTTCTTGGACACTGGGGCTTCTGTGCTCGACACGCGCAACATACACCGATCTGTTGTCAT
 GAGGACCATCATGAGACTCACAATTTCCCTCTTGTGAATTTGCAACTGGCTTCTAGAGACTTTGATCTCA
 ACACAGACCTTACCAGCTGATGAATGCACTGAACACACTGGACAGGATGTCTCAACAGCTACACGTACAG
 CTCATGGAGCTGAGGAGCTGCAAGGTTTACAAGCAGTGTACCCCGGACTCGAACATGGACCTGGATGGAG
 AAGCTATGAGCAATACAGGCAATTCAGCGTCAAAAGTGGCCACAGACTGTCTATTGGCCAGGAGGCTCAGTAAGC
 GACACTGTGGGAGGCTGGGAAGGTTAAGAAACACAGAGGTGGACTCCAAAACATAGAGGCTCAGCTGA
 CTGACAGAGCTGAATAACATGTGGTGATTTCACAGACTGTGCTATTGGCCAGGAGGCTGACCAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACACAGCAGGAGCAGAGATTAATCTCAGGAAGTCC
 ATTTTGGCCCTGCTTTGTTGGATTATACCTCACCAGTGCACAAAATGCATTTTTCGATATCAAAAGTCC
 ACCATACCCCTCCCCAGAGCTCACAAGGAAACCGGAGAGAGCGAGCAGAGAGATTTCTTGGAAATTTTC
 TCCAAAGGCGCAAGTCAATTGGAATTTTAAATCATAGGGGAAAGCAGTCTGTTTCAATCTCTTATTCTT
 TTTGGTTGTCAAGAGAGGAATCAAGAGCAGGACAGAGGCAACGTTGAGAGGCTGAAAACAGTGCAGAGAGC
 TTTGCAATGAGTCAGTAGACCAAAAGAGATGACATTTACCTAGCACTATAACCTCGTGGTCCCTCTGAAGAAA
 CTGCCTTCATTGTATATATGTACTATTACATGTAATCAACATGGGAACCTTTAGGGGAACCTAATAAGAAAT
 CCCAATTTTCAGAGTGGTGTCAATAAACGCTCTGTGCCAGTGTAAAGAAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRENIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMPHRPVLNVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQKRKLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVPFYVRGPNVEAGCLNPHIVLNIIDLAPTIIIDI
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAI EVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYIILENDTVQC DL DLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRP EECDCCHKISYHTQHKGRCLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNN DTC SMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWC MRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCA**GATG**CTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACC
CCCCGCCACACCCCTACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
CGCTCGC**TGA**GGCTGCTGTGCGCGGTGCCTGTGGACAGCAGTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGCTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFRR
RRGHLGIFHHHRHPGHVSHV PNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 50

GCGCGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCITTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAAGTGTGGTCAACCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCACATGTTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCCACTGGCACGGCAGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
 CTGGCAGCGCGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACAGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCGAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTCACCTGGAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCACAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSVSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
 GCCCCGCGCCAGT**CATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGCTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAAT**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETILVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACCTGGCCTATGG
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACCGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTGTGTTTCTTGGCTAAAAATCGGGGGAG
 TGAGCGGGCCGGCGCGGCACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGCGAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACAAAAATCTATTGTGGTATGCACCTTGATTAACTT
 ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTGCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCGGTGG
 TCAAAATCTCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGCTCTCCGCTGTGCCTCTCATTT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCATGCGGATTCCTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCGGAATTNCTNTATTTTTCCAGAATGCC

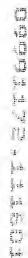


FIGURE 61

TAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGAAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCCTAATGATTAAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCCGCTGGTGTCTGCTCTCGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGATTCTTACCTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAGCGCCCGCCAGCCGCTTGTAACTGACAAGGAGGCCAGGAAGAGGTTCTCAAACAAGC
TTTTTTCAGCCAAACCAAGTCCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCCTGGTGTCTGGAACAACAT
ACCAGGAGCAGGGGGGCTGCTGTCAATCCTTTGGAAAGAATGGCCTGTAATTGACACAGGAAT
CCATTAGATTGGGCTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCGAGTACTG
AAGGGCCAGCTGCAGTGGGCTCCCTGTCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAGAGGATACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGGCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
AGTGGAGCCCTTGCCTGCTGTTGAAATTCCTCCATTGCCCTGGTTACGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCATTCCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCGAGCAGCTGGGGGCTTCTCTGAGCTCCAGGCAGTACTAGCTACATCTTCCCCA
CTTACGGGTGTCACCCCAACCAAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC
ATGAAGAGGAGCTTTTATCTCCCGAGGGGTTTCCAGTGAATTCCTTCCACACCATCCTGT
GATTACGGGGGCTGGGGGCTGTCTCTCAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCTATGGTGGTCTCCCAACGAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCTTGGCAGGTTGTGAAGCAGCAACTGGGGACGGTGGCGCCGGCTTAGCGGTGACCT
CTGTTTTTCATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCCTCCACCAACTACAT
GTTTACIATGACACGACATGGACCAGGCGATGGAGCGTACGTCCTCATGCCCAAGGAAGA
GGCTGCCGAACACATCCCTCTTCTCTTCTGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGCGGCTCCACCATGATCATGCTCATACCACTGCTTACGAGTGGTTT
GAGGAGTGGCAGCGGAGCTGAAGGGAAGCGGGGCGAGTACATGAGACCTTCAAAAACTC
CTTTGTGGAAGCTCTATGTGCTAGTGGTCTTGAACCTGTTCACAGTGGAGGGAGGTTGG
AGAGTGTGACTGCAGATCCCACTCACCACCACTTCTATCTGGCTGCTCCCCGAGGTGCC
TGTACGGGGGCTGACCATGACCTGGGCGCCCTGCACCCCTGTGTGATGGCCCTCTTGAGGGC
CCAGAGCCCATCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTCTG
GGGCGCTGCAAGGTGCCCTGCTGTGCAGCAGGCCATCCTGAAGCGGAACCTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAGAAAT**TAGT**TCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCCTTTCTG
CATTAGTTCTTGACAGCTATAAAGCACTCTAATTTGGTTCTGATGGCTGAAGAGAGGGCTAG
TTTTAATCAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGTATG
GGTGCATGACGAGGGGCTCTGCATCCCTCACCCTGCTTCACTCAGTCAATCAAGCGA
TATTTCACTCTGTTGATAGAACCCTGGCAGTGTGTCACTCAACCTGGTGGGTTCAGTTCT
TGTCTCAGGCTTCTGCTCTCATTCAATTTAGTGTACGTCGACAGTCTACACTGTCAAGG
GAAAGGGAGACTTAATGAGGCTTAACTCAAAACCTGGGCGTGGTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAAGTGGCTTTCAGGGGACAGGAAT
GCCCTGTCTGCGCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCTCTGAGATGCATATCCAATTCAATATGGAAGTCCCGGGCTGTCTCTCCTATCA
CTGGGCTGGCAGCTGGTTCTCAATGTGCCAGCAGGGAAGTCACTACCTGAGCCTCAATCAAGC
TCTTTCCACCAATACACAGGGAAGGGTGTGAGGGAAGGGGATGACATCAGAGTCAAGGCA
TGGACTGGTAAGATGAATCTTTGCTGGGCTGAAGCAGGCTGCAAGGGCATTCAGGCCAAGGG
CAGCAGCAGGGAAGTGTGAGGAGGTGTGGGTAAGGGAGGGAATCAGATCAGAAAAGGGA
AAGCCAGGGAATGTGTGAGGCCAGAAATGGCAATTTGAGTTAATTAGCATGTGAGGG
TTAGACAGGTAGTGTGAATGCAAGCTCAAGGTTTGGAAAAATGTTTCAAGTTATGCTCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

FIGURE 64

MWLPLVLLLAVLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPiVVSNAglFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTkEDLHLPSTNYVYVYDTMDMQAMERYVSMPREEAAEH
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAKKKK

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGAGAGGAGGATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGTTGCTGCTGAGCTTGGCCTCGGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTCTGTATGCCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAAGGCTCTTGATAT
 ATTATACATTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAAGACCAATATTCAGTTGAACCTCCTTCAA
 ATCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTAAATTTCTCTGAGTTGGAATTGTGAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTATTCTGGTCATTTATTGCTAGTGACACTGTGCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATTTTTTAAATAAA
 ATTATGTCTAAGATTAAAAA
 AA

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCCTCGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

Q
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FIGURE 69

GCCGCCGCCGCCGAGACCGGGGCCGGGGCGCGGGGGCGGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGCAGCGCGCGGGCCCGGCCCTGACCCCGCGCCGCCCGCTGAGCCCC
 CCCGCCGAGGTCGCGACAGGCCGAGATGACGCGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCCG
 CGCTGCTGCTGGGGGCTTCCCAACCGCGCGCGCGCGCCGAGGCGCCCCAAAGATGCGGGGAC
 AAGGTGCTCCACGCGAGGTGGCCGGCTGGGCGCGCACTGTGCGGCTGCAGTGCCGATGCTGGA
 GGGGAGCCCGCGCGCTGACCATGTGGACCAAGGATGGCCGACCATCCACACGCGGCTGGA
 GCGCTTTCGCGCTGTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGGCG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGCTCAACTACACCTCGTCTGT
 GCTCGATGACATTAGCCAGGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTTGGGGGTCAAG
 AAGAGCCCGCGCAGCGCAGTAGTGGGCACGACCGCTTACACAGCCCTCCAAGATGAGGCGCG
 CGGGTGATCGCACGCGCTGGGTAGCTCCGTGCGGCTCAAGTGCCTGGCCAGCGGGACCC
 TCGGCCGACATCAGCTGGATGAAGGACGACCGGCTTGACGCGCCAGAGGCGCTGAGG
 CCAGGAAGAAGTAGGTGGACACTGAGCCTGAAGAACCCTGCGGCCGAGGACAGCGCAATAC
 ACCTGACCGGTGTGAACCGCGCGGGCGCCATCAACGCCACCTACAGGTGGATGTGATCCA
 GCGGACCGCTTCAAGCCGTGCTCACAGGACGACCCCGTGAACACGACGCTGGACTTCG
 GGGGAGCCAGCTCCTTCCAGTGAAGGTGGCAGCGAGTGAAGCCGCTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCGGAGGGCGCCACAACTCCACCATCGATGTGGGCGGCCAGAA
 GTTTGTGTGCTGCCACCGGGTGACGTGTGCTGCGGCCCGAGCGGCTCCTCACTCAATAAGC
 TGCTCATACCCGCTGCGCGCAGGACGATGCGGGCACTGTACATCTGCTTGGCGCCAAACCC
 ATGGGCTATCCTTCCGACGCGCTTCTCACCCTGCTGCCAGACCCAAACCGCCGAGGGCC
 ACCTGTGCGCTCTGCTCCTCGCCACTAGCTGCGCGCTGGTCTCATCGGATCCAG
 CGGCGCTGTCTTATCTTGGGCACTGCTCCTGTGGCTTTGCCAGGCGCAGAGAAGCGCC
 TGCACCCGCGCGCTGCCCTCCTCCTGCTGGGCGCGCGCGGGGACCGCGGACCG
 CGAGCGGACAGAGGACTTCCCTCGTTGGCGCGCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGACATGGTCTCGGCGAGCCCCCAGCACTTCTGCGCCAGGCGCCAGTTGCTGGC
 CTAAGTTGTACCCCAAACTCTACACAGACATCCACACACACACACACACTCTCACAC
 ACATCTCACAGCTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGCAGCAGCGCACCGT
 ATCTGACGTGGGCGCGGGGGCGCGCGCAGACAGGAGCTGGGAGGATGGAGGACGAGCT
 GCAGACGAGGCGAGGGACCCATGCGGAGGAGGAATGGCCAGACCCCGAGGCACTGTGTGT
 TGAGGCTATAGCCCTTGACACACACACACAGACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACAGCTGCTCCTGAAGGCACACGTACGCACACGCATGCACAGATATG
 CCGCTGGGCGCACAGATAGCTGCCAAATGCACGCACGACAGAGACATGCCAACA
 TACAGGACATGCTGCTGAACATACACAGCACACCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATTAATGTCCTTGACACACATGACCG
 ATATTGCTGGACACACACACACACACCGCTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCGAGATATGCTGCTGGACACACACTCCAGACACAGTGCACAGGCGAGATATGCT
 CACTGGACACCGCAGATATGCTGTCTAGTACACACACACGACAGATGCTGTCCGGACAC
 ACACACGATGCACAGATATGCTGCTCGGACACACACGACGACAGATATGCTGCTGGAC
 ACACACAGATATGCTGCTCAACACTCACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATATGCTGCTCGGATACACAG
 CAGGCACACATGCGAGATATGCTGCTGGGACACACTTCCGGACACATGCACACAGGT
 CGAGATATGCTGCTGGACACACACAGATTAATGCTGCTCAACACTCACACAGTGCAGATA
 TGTGCTGGACACACACATGTCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA
 TGCTGCTGGACATACACGACGACACATGAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTCAGATATGCTGCTGGACACGACAGCTGACGTGCTTTTGG
 GAGGTGTGCGCTGAAGCCTCAGTACGTGTGCGGCTGAGGCTCATAGTTGATGGGAGCATTT
 CCGCTCTCACCCTCACTCCCCAACTCTGCGCGCTCTGTGCCCGCTCAGTCCCGCCCTC
 CATCCCGCTCTGTCCCTGGCTTGGCGGCTATTTTGGACACTGCTTGGGTGGCGGACG
 AGTCCCTACTGTGTGGGCTGGGTTGGGGGACAGAGCCCCAAGCTGAGAGGCTGGAG
 CCGATGCTAGTGCTCATCCCCAGTGCAATCTCCCCCTGCACAGAGAAGGGGCTTGGA
 TTTATATTTAAGATAAAGATAATTAATAATGATGAAGGAAGACTGGGTGTGAGGAC
 TGTGTGCTCTCCCTGGGCGCGGACCGGCTGTCTTTACGCTATGCTGATGACACACCC
 GTCCAGGCGACACACCCCGCCACCCACTGTGCTGGTGGCGGCGAGATCTCTGTAATTTTA
 TGTAGAGTTTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

1053112140501
 1053112140501

FIGURE 70

MTPSPLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDISP
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITW
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKP
VGTHPVNTTVDFFGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLP
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSS
TSLFPWPVIGIPAGAVFILGTLLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGSAPAQHLLGFGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

FIGURE 71

CCACGCTGAGGAGGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCAGGGGACCGCATTCCAGAGTC
AGTGACCTCTGTGAAGACACCACATCTACCTCTTGCCACGTTCCACACGGGCTTGGGGGAAACATGGTGGGAGCCA
AGGCTGGGTGTTCTCTCTCTGGTCTGGGAAGTCACATCTGTGTTGGGAGACACAGCATGCTCACCCAGCTA
GTAAAGAGATCCACGCTGGGAAGAAAGAACCCAGCATCTTTGCCAAGCCTTGGCAGACCCCTGGAGAGCCCTGG
TGAGTGGACAACATGGTTCAACATCGACTACCCAGGCGGGAAGGGCGACTATGAGCCGCTGGAGCCCTTCGCT
TCTACTATGGGACCGGTGTATGTGCCCTGCCCTGCGGCTAGAGGCTCGGACACTGACTTGGACACTGCGGGC
ACTCTGGCCAGCATGCTGTCTGATGTCCTGCGGCTGGAGGTTCTGCTGGCTCAAAAGCAGTGGAGGCTGGCA
GAACTGCTCTAATTACACCGTAGCTTCTCTGCCACCAGGATCCCTCGCGCAGACACAGAGCGCATCTGGA
GCCCATGGTCTCCTTGAGGACAGAGTGTCTCAGCTGCCCTGTGGTTCAGACTGGGGTCCAGACTTCGACACGCATTTGC
TTGGCAGAGATGGTGTCCGTGTGCACTGAGGCCAGCAGAGGGGTGAGCACTGCATGGGCGAGGACTGTACAGC
CTGTGACATGACTGCCAATGGGCGAGGTGAATGCTGACTGTGATGCTGCATGTGCGAGGACTTCATGTCTTC
ATGGGGCTGTCTGCTCTGCTGCGAGGTGCCCGACCTCAGGGGCTGCTATCTACCTGACCAAGACCGCCAGG
CTGCTGACCCGACACAGACAGTGTGGGAGATCCCAATCCCTGCCCTGTCTGCTGTATGAGCAAGGCTTCCTGA
GATCAAAAGGTCAAGTTGCCCCCATTTGTACTCAAACTGCCAAGACTAGCCTGAAGGCGACCCACATCAAGG
CAGAGTCTTGAGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCAGGAGAGCTGGGAGAGG
GTGTCTCTGTGCTGTAAGGCCACAGGGAAGCCAGGCCAGACAGTATTTTGGTATCATATGAGGATTCGT
GGATCTTCCCTTCAACAGCATGAGAGCAAGCTGTGTCTGAGGAACCTGCGAGCAGCCAGCTGGGGAGTACT
TTTGCAGGCCACAGATGTGCTGGGGCTGTGATTCAGGTTGCCAGCTGATTGTACAGATCTGATGAG
ACTCTTGCACACCAAGTCTCTGAGAGCATCTATCCGGCTGCCCAATGATGCTTTGAGATCCGACCAACTCT
CTTCTACTATGACCTGGGACGCTGCCCTGTAAAGACTTGTGAGGCGACGAGATAATGGGATCAGGTCGGTG
ATGCTGTGCGACATGCTGTGGCATCTTCCAAAGACAGAGGAAGGGAGATCCAGTGCAGTGGCTACACGCTACCC
AACCAAGTGGCCAAAGGATGCAGCTGCCAGCGGTGTACGGAAACTCGGAGACTCTGTGGGGGCGCTGTGCTGT
TGCTGACATGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCCGCTGAAGCATGACTGGCTACA
AGGGCATCTTACCTCTCATGTCCCGAGACACTGAGAGGCTGTGTCTCACATTTGTGACAGGCTGTGACAG
TTTGTCAACACCAACCAAGTGTCTACCTTTCAACAAGAAGGGAGTGGCGTGTTCATGAATCAAGTACTGCTTC
TCGGAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCTCTGGGGGAGTGGTGTGGTGAAGACC
CCATGGCTGAATCGTGAGATTCACTCCAGGATTTCTACAGGCAAGTGGGAGGCCCTACATAGGAAGAAAGTGAAG
GCCAGTGTACCTTCTTGATCCCCGAATATTTCCAGGCCACAGCTGCCAGACTGACCTGAACCTCATCAA
TCGCAAGAGGACATCTTCCCTTTCGGACGATGGCATGTCTCTGTGGATTCAGAGTGAAGTCACTCACTAG
AGCCATCTTAATGCTGGCAAAGTGAAGTGCACCTTGCTGGACCCAGGTCAAGATGCGCGAGCCATATGCCA
GTGAACTCTGTGCTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAGGTGATTTCAAATTTGAAATCAAAG
GAGGAACCAAAGAGAGACAGACAACCTTCTGGTGGGCAACTGGAGATTCTGTGAGAGAGGCTCTTTAACTGG
ATGTTCTCTGAAGCAGCGGTGCTTTGTAAAGTGAAGGCTACCGGAGTGAGAGGTCTTGTGCTAGTGAGCAG
ATCAGGGGGTGTGATGTTCTCGTGAATTAACCTGGAGCTTGAACCTGCCCTTCTGCTCCAACTAGGCCCTGGG
CGCTTTGACATGCTATCACAGGCCCAAGGGCGCTGTGTGCTGCTCTGTGCTGCTGCTGCTGCTGCTGCTG
CCTACTCTGCTTATGCTTGGCAAGCCTGGCTGGGAGGAAGTCAAGAGCTGGAGTCTTCTCTAAATTCAC
CCAAATGCAATTTGGGCTCCCTCAGCCCTATCTCAGCAAGCTCAACTACCTGCGAGCGAGCATAGGATCCAGC
GGTTAAAGAACAGCAGCTTTCCAGATTAGCATGCCAAGCCCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCA
TCTATGCCCTTGAGAACTCCGGGCACTGTGAAGGGCACCCACAGTGCAGCCGCTCTCGGTTCTTACCAAT
GAGGGGATCGATATGACACACACAGTCCCTTCAACAGAGTGAACCTGACCTGCTGACTGAGCATCTCT
GGCATGTGGGCCAAAGCCGATGGAATTCAGGGCCTGCTATATCAAGTGAAGATTTGGGGCCACTTGAATGGA
ATGTGCGATCCCGAACATGGGGGCACTCATCGCGGACAGTGGGAGGCTGTATGGAATCCGAGATCCGATGGA
AGCATCTGGGACAGGGACAGGCCAATCTCTCAGCTGCCTGTCTGGAGTCAAGTGCAGTGGGATGCTGTATGA
TCAGGACCGTGTGGACGCACCTCGTGAAGGTCATCCCGAGGGCAGCTGCGGAGCTGCTGTGTAACCCCA
TGCTGATGAGTACTGTGCTGACCTTGCACCTGACATCAACAGCAGCAGCTGAGTACACATGCTGGCA
CCCTGTGACCTGAGGCTGGCCAGCACTATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
CGCGCTCGGCGGTGCTTTGATGGCACATCCGATGGCTCTCCAGAATCTGAAGAGCAATGTGGGAGTAGCC
TCACCTTCACTGTGTAGAGAGGCAAGTAGGCGCGCAGATGCCCTTCCAGTCACTCAAAGCAGCCAGCCGAC
TCCCTCTGCTGAGGCATCTTCAAGGAAGATGCCCTCGAGGAGGACAGCAGGAGGAGGCTGGCCAGGCG
CCAGGGTGGAGTGTGGCTCTGTGAGATTTCTAGAGTTGCTCAGACGCCCTGATCAACCTAAATTTGTGGT
ACTTCCCTCTGCT
TTAAGCACTTCTGTTTCTGGAATTTGCTTGTGTTTCTTCTGCTTCTTACTTCTTGTGCTGCTGCTGCTGCT
TTGGCAGCTGGCGCCCAATGGCACATAAAGCCCTTTTGTGAACCTGTTCTTTAAATGAACACAGAAAT
GGCCACTGTTAAATCTGCGACTTCAACTGTACTTCAATGCCATTAATGCAATTAATCTCTCTCTCTTCT
TTTGGTCTGTTTGGCCACTCTGCAATAGTGATATCTGATGCTGAAGATCAAAATAAACCAATATAAGCATAT
TTCTTGGCT
AAATAAACACAAATCTTTACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATCCATCAAGTTAAGCTTTAAATATAGGGTGATCATAGTTCTCTTACCAGTCTGGAAAGCAACTCTCTGTT
ACCAAAATACACCAAGTTGCTAACTGATTGTACATTTCCCTTTGCAATTCGCTTTTGTCTTGTCTGTAAGC
CCAGTGTAGCCAGGGCAGATGTCAATAATGCATCTCTGTATTTGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMILTQSVRRVQPGKKNPISIFAKPADTLESPEGWTTWFNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGGVVHGSPEGFWCLNREQ
RPGQNCNYSYTVRFLCPPGSLRRDTERIWSPPWSPWKSACAAGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
TPKLLTQTDSGGRFRIPGLCPDGKSILKITVKVFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPESYLIRLPHDCFQATNSFYDVGRCVP
KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKECSCQRCETETRSIVRGRV
SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELIPSRSFYRQNGEPIYIGKV
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRRCFVKVRAYSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGFNGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPAIAGVPQPYLNKLNRYRTDHDPR
VKKTAFAQISMAMPNSAEESNGPIYAFENLRACEEAPSAHFYQIEGDRYDYNTPFN
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPQGSRRASVNPMLHEYLVNHLPLAV
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCDFGTS DGSSRIMKSNVGVALT
FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTTCATATTTGGTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCCTACCTACCGTAGCAGCATACATATGTGTATATATGTAACCTAGACAAAAGATCCGAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAAGAAGATTACAAAGAATTTAGACATGTTATTTGTCGAAGATCCCTGCGATTATG
 CCCTTTGGGTTTACGGTCTCTCAGTGATGCGAGCCCTACCCCTTTGGTTTGGGGACATTATGATTTGGTGAAGACT
 CAGATTTACACGGAAGAGGGAAGTTTGGGATTACATGGCCTGCGAGCCGGAATCCACGGACATGACAAAATA
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTCGAGACGTTCTGTGCAATGSGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCAGACACCCCTGAGCTGATGTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTTGGAAGGAGTATCCCAAGCCCTCTCCAGGTTAAACAT
 CACTCTGCTTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCTCGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTGACACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAGACAGGTTCCGGCTTTTGTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACACCAAGAAACTCAGAGATTTCTTT
 ACAGTACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGAAATATTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAAACAGCAAAATGACATGCGAATGTGAGCACAACTACAGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGGCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAACTCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACAGAGCTCCTGCACTGCCAGAACGGAGGACGTGCCACA
 ACAACGTGCGCTGCTCTGTGCCGGGCCGATACACGGGCATCCTCTGCGAGAAGCTCGCGTGCAGGAGGCTGGC
 AGCTGCGGCTCGACTCTGGCCAGGGCGCGCCCCCGCAGGCACCCAGCGCTGTGCTGCTGACCAAGCTGTCT
 GGGAAACGCCAGCCCCCTGGTGTTCTAGGTGTCACTCCAGCCACACCGGACGGGCTGTGCGGTGGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACATTGGCAGCTCGAGAGCATATTGTGGA
 TTGGAAGGCTGCGCAGCCCCCAACAGGAAAGACAAAAACAAACAAATCAGCCGACCTAAAAACATTGGC
 TACTCTAGGCTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTCTTTGCTGTGAG
 GTGCAATTGTGGGCAATAGGAAATCTGTTTACAAGCTGCCATATTGGCCTGCTTCCGCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTCTTTGTGCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCTAAAGGGCAAGCCAGTCTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCCATATACAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCCTTTGTATTCAAAATGAAGTT
 ATTTTCTTGAACACTCTGTAATATGTAGATTTTTGTATATTGGCAAATTTGTGTTACCAGACAATCTGTTAAT
 GTATCTAAATTGAGTACGAAAGACTGACATTTTATTGTTCTCTTTGCTTTCTGTTTGTTCCTGTTGTTCACTG
 GATTTCTCTGTAAGGCAACAGCTGCTGGCATCAAAGAATACAGTTTACATATATAACAGAGTATATAAGA
 TTTCCACCAAAGACATCTTAATGTTTTCTGTTGCTTTAACACTGGAAGATTTAAAGAAATAAAAACTCCTGCA
 TAAACGATTTCAGGAATTTCTTATTTGCAATTTCTTAAGTAAAGGAACAGCACCAACAGCACTTTACACACT
 TTACTGATTTCTGTGTGGACTGAGTACATTCAGCTGACGAATTTAGTCCCAGGAAGATGGATTTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTTGGGAAAAATTAACACAGCAAAAAAATAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISISIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRC EEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGTTCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT
 CTCTTTGTGGACCA**ATGT**CCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCC**CT**ACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCCAGTATCCAGGTTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTTGGAGACCCCTGTGGTGGGAATTCACAGCTTCTTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTCAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTCGAGGAGTTACCTTGCAGAACATTTCTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCG**TGA**GGCCAGCCACCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTCGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTGCCCACAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTATGATTTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT
 TTACTTTTACATATTCGTTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATAAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFFAFCVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTTCIGLASRPYAFLEFDSIIQVKVK
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

FIGURE 77

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGA
 CCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGT
 CCTGCCCTTTAAGGGCGGGGCGTCCGGAGCACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCCCGGGCCAGAGGCACCTCGGCTTCAGTATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGC
GAGTGATTATATCAACACTTCTGTTTGC AACACTGTACATCCTCTGCCACATCTTCTGTAC
CCGCTTCAAGAACCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGCTGCTGCTGCTGCCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCTCGGAAGTACTACATCCAGTGGCT
CAACGGCTCCCTCATCCATGGGCTCTGGAACCTTGTTTTCTCTTCCCAACCTGTCCCTCA
TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACCTTACTCATGCACTCTCCTTCTTGGGGTTCTG
CTGCTCCTGGTGTGTA CTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACCTGGGAAGCTGCT
AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTA CTGCTCAGCCTTTGAGGAGG
CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
CTACACAGACAGGTCTTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGCGGAAGGC
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGG
GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
CCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
TGCCGTCACTCAGGTTGTA CTCTATCTTTACCTAATGGTGTCTCAGTTGTGGGGTCTATA
GCTCTCCACTCTTCCGGAGCTGCGGCCAGATGGCAGCACTGCCATGACGCAGATAATT
GGGAAGTGTGTCTGTCTCTGGTCCCTAAGCTCAGCACTTCTGTCTTCTCTGAACCCCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
TTGTGTTCTCTACACGCAAGCCTTTGAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGTGCCCGT
CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGCACTCCAGCTGGGGGTGGGA
AGGAAAAAAGTGGACACTGCCATCTGTGCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGAGCAGAGCCATCTGCACATT
GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACCTGTGGCT
CAGCATGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
ATCTGCCCTCACTGCTGTTCTGGGGCCATCCCCATAGCCATGTTTACATGATTGTATGTGCAAT
AGGTGGGGTAGGGGAGGAAAGGACTGGGCCAGGGCAGGCTCGGAGATAGATTGTCTCC
CTTGCTCTGGCCAGCAGACCTTAAGCACTGTGCTATCTGGAGGGGCTTTGGACCACTTG
AAAGACCAAGGGGATAGGGAGGAGGAGCTTACGCATCAGCAATAAAGTTGATCCAGGGA
AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPSIIISNEVLLSLPRNYIYQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLG R VYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQ R V L L E K R R K A S A W Q R N L G Y P L A M L C L L V L T
GLSVLIVAIHILELLIDEAAMP R G M Q G T S L G Q V S F S K L G S F G A V I Q V V L I F Y L M V S S V V G F Y
SSPLFRSLRPRWHD T A M T Q I I G N C V C L L V L S S A L P V F S R T L G L T R F D L L G D F G R F N W L G N F Y
IVFLYNAAFAGLTTLC LV K T F T A A V R A E L I R A F G L D R L P L P V S G F P Q A S R K T Q H Q

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTCTAGCTGCTGT
GGGTGATATTACTGGTCTGGCTCCTGTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC~~TAG~~GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAAGTACTCCAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACACCCAGCTGGGCGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAGTGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTCGGAAGAAAGATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTTCAATCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRKQYD TYGEEGLKDGHQSSHGDI FSFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVDCPCPNVKLVNEERTLEVEIEPGVRDGMETPFIGEGERPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCCCTGATGATCCACAAGCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

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METVIVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSSEL
 ELDDVVTNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
 VSDIIVAKRISPRVDVVKSMYPPLDPKLLDARTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREALASEPDKLGPPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTGCGCGCTGTCC
CCACCCTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGAGTGTTTTTCTGTCTTTGGAATGATTCCTTTTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTAGAAAGAACATTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
GGGCTTCTTTCCTGTCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTTGAAGACTCATTTAAATATTGTGTATTTATAAAGTCATTTGAAGAATATCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAAGGCTATTTGTGTGTTTTTCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCAATTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTGNCNCAGGGCC

FIGURE 90

MISLTDQKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLPGL
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGTTTCTAAGTCCATGTGCCAAA
GGTGCCAGGAAGGAGACGCCCTCCTGAGTCCTGGATCTTTCTTCTTCTGGAATCCTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCTGTGCCACCTGGTCTTCTGTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTACAGTCTTCACTCTCCTCCTCTGGCCATTAAACAGCAGCTCTTCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCAACGAGATGTTCTTCTGTTGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTT
GATTCAGTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTACAGCTGTATATGACTGTACACTCAATTTTCAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCCTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAAGTGGCTGTTTGGGCCCTCGC
TGGTGCTTACCTTTCTTCCAGTTCCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTCAACATCCGAAGGGAACTTGGGGAAGTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCCTGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTAAAAGTGCTTTAGGTGAGATGACTAAATTTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGTTTTCTTCTTGGGGAA
 GTAAAAGTGAGCCAAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGATCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAACACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACCAACCACCTCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTTACA
 TTT**TGA**TCCTTTTAAACCTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCCTTAGAATTGGAAGAGTGAAGACAGGACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCACGTAATTGAGACCATGTCTATTAAAAAATAAATGGAAGACGAAGAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTATCTGAGTCATTAAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAA

MEGESTSAVLGGFVLGALAFQHLNTSDSTEGFLLGVEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITFESCSTRLEHSLYKPKQGLFHRVPLVAVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEEELKSICKKVEDESEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENITFCQALRITFFPNSEFLHSCVMSLKNRHVSKSS
CYNHHLDDVNDLTLMEVHTDIEPASFSTPQCIKKHALDLDWRWQFKSRLLDTQDKRKA
NTGSSNQDKASKMSSPTEDEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGTCAAGCCGAGCCGAGTCCAGCCGAGCAGCGGACCAGCGCAGGCGCAGC
 CCAAGCAGCGCGCAGCGAAGCGCCCGCGCCGACACCCCTCTGCGGTCCCGCGCGGCTGCCACCCCTCCCT
 CCTTCCCGCGGTCCCGCGCTCGCGCGGCAGTCAGTCTGCCGGTTCGTTCGCGCGGAAACCCGAGGTCAACA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGGCACC
 GGGGACCGTTCGCTGACGGGAGGCGCGAGCTCTACTTTTCGCCCGCGGTCTCTCCCTGCTCTCCCTCTCCAC
 CAATCCCACTCCTTTCTCCCTCCAGCTCCACTCGCTAGTCCCGACTCCGCGACCGCTCGGCCCGCTGCGGTAG
 CGCGCTTCCGCTCCGCTCCCAAGTGGGAACGCTCCGCCCGCGCGCACCTGGCAGCGTTCGGCTTGGC
 CGCGCTTCTCTGACCCCTGGCAGTGTCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTCGCGAGCTCTTTACGCTCCAAAGGCTTCAACAAGACGATGCCCGCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCTGCCAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGGAAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAAGTTTG
 ATGAATTCCTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTCGAGCTATTTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAATTTGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGGTCTCGTGTTAAACCCACAGCCCGAGTGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTCTTCAACATTGAATCGGTTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTTGAACATCGAGG
 ATAATAGTGTTCAAGTGCTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTT
 TCTCGTTCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAAACCAACCAAGC
 AGCTGGCACTAGTTTGGACCGACTGTTTACTGATGTCAAGGAGAAATGAAACAGGCCAAGAAATCTGGTCCT
 CCCTTCCGAGCAAGCTTGCACAGATGAGAGGATGGCTGCAGGAAACCGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGATTAGCCAACAGGGCAACCAACCAAGGCTCA
 GGTGACACCAAGCAACCAAGACATACTGCTTCAATCATGGCTTCGCGATGATGACCAAGAGTGGAAATGA
 AGAATGCATACAATGGGAACGACCTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAAGAGTGGAAATGA
 GGCTGTGATATCAGCAGTGCCCTTCAGAGTTTGACTACATGCCACTGACCATGCTGCGAAGAGTGGCAATGA
 GAAAGCCGACAGTGCTGGTGTCCGCTCCTGGGGCAGCGCTACCTCCTCAGTGTCTTCTGATCTTGTTCCTGG
 TTTATGCAGAGAGTGGAGATTAATCTCAAACCTCGAGAAAAGTGTTATCAAAAAGTTAAAAGGCCACCGAGTT
 ATCAGTTTCTTACCATCCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTTACTATGTGGC
 CACTGGTTTAAAGAGTGCTGACTTTTGTCTCATTGAGTTTGGGAGAAAAGGAGTGTGCAATTGAGTTGGT
 TCCCTCTCCCCAAACATGTTTAAACGTTGGCTAACAGTGTAGGTACAGAACTATGTTAGTTGTGCAATTGTGA
 TTTTATCATCTATTATTGTTGTTGATGTTTTTCTCATTTCGTTTGTGGGTTTTTTTTTCCAACTGTGATCT
 CGCCTTGTCTTACAGCAAAACAGGCTCCCTCTTGGCAGTAACATGACGATTTCTGAAATATTAAATA
 GCTGTACAGAGCAGGTTTATTTATCATGTTATCTATTAAAGAAAAAGGCCAAAAAGC

MARFGLPALCTLAVLSAALLAAELKSKSCSEVRRLVYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEELYSLSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLSNDM
VKTYGHLMYQNSLFDKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHRCGLVTVKPCYNYCSNIMRGCLANQGDLDFFEWNNFIDAMLMVAERLEGFPNIES
VMDPIDVKISDAIMNMQDNSVQVSQVQVQCGCPKPLPAGRISRISISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNAGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAOAYLLTVFCILFLVMOREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCATTATATCTCTCAA
GCAACTTACAGCTGCACCGACAGTTGCC**ATG**AAAGTTCTAATCTCTTCCCTCCTCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAGGCACACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTGTGTTGTGCTCTC
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGC
AATCAGGAAAGTAGCAACAGAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA



PODCAST

[illegible][illegible]

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGTGCTGGTGTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTPLPLHMLLGCWQPLCKSYFFYLMVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGP HIMGKAVKQSF P
SSKALICSFPSLQLEQATHQPIY LPLRGT

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAAECTTCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCGGTCCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTAGCCTCTACTAAAGTTGTTCATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAAACAGGCAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTGAACTGTAAGCAAGCATTCTCAG
 GAAGTCTCGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTGTGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAALLHWNHGLKWPWGRTASYTDVWEKWYIPDFTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCATAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTCCGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGTTACAGATTAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGTGCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCATAAATTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCACAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACACAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGTCAAAC
 CTGACGGAATGGAACAGCAGAATATAACTAACCAACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCGCCACCTTGGTTCCAGT
 GCTGGAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAATAATGGTATATTCCA
 GACCCAACAGGCAAAATTAACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAATTTGAACGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGTACCTGC
TGCAGCCCTGAAGGCCCTTGGCCTAGCCTGGAGCCCAGGACC~~TAA~~GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAA

FIGURE 109

MGA AISQGALIAIVC NGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGFWPSLEPRT

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCATCTGTTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGGAAATAAGCCCCCT
 TTCGGGCAATTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATCA
 TCCTTGCGTGCCAGCAAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAATGCTATTAAATGGGACAGATTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTTCTGTGTTTGTGCTGTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGATAGATATCCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAAATTTTTTTTTAAAGACCTAATAAACCTATTCTTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTTLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFAlVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAAATATTCATCTCG
 TGTGGTGAAAAATTTTGGAAAAAAATTTGCCCTTCTTCAAACAAGGGTGTCTATCTGATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTGCTGG
 TGACTGGAGTACATTCAAACAAGAAACGGCAAGAAGATTAAAGGGCCCAAGTTCACTGTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCCAAATACCATGTTATGGCACTGAGCTGTATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTGAGAGGGAAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATCCAACGGTGTCCAATCGTT
 ATCCCTTACCAGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCTCTCTG
 CTGCTTCTACACAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCTCCAGAAACCTGTTGGAGCGGATGTCAAGCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCAGCATGGCCAAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCGTTCCAC
 TGATGGGTGTGTCCAGATGTGAGACAAACCTGCTACTCACTTTAACTCAAGACACACAGC
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCCGGGCCATCTCCTTTGTGACCAGAAGTCTTTTCCAAAGCCAATGGAACAGAAAGG
 GGGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TCAAGACTTGGCAGAGAGTCAAGAAATCAACATTTCTTCACTCACCATTGAAGTGTGCTGA
 AATGACAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAGGCGGTGTGCAAGCAAAAG
 GCTTCTACTCTCCACCTGCAGAGCTGGGTTGGCCCTCCCAAGACCTGCAGCGCTTGGTG
 AAGCGGTCTCGGACACTGACCCCTGGCTGGAGTGGTGGCAGCAGCAGCGGCTGCCATCA
 TGCTTCTGCTATCGACGGCTCCAGCAGTGTGGGACGGGCAACTCCCGACCGTCTCTCCAGT
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCCAGCAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCAGCAGCAGCGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAGGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGAGGTCCTACGACGACCTCCGGATCCAGGCCATGGCTGCCATCTGAAGGG
 AGTGATCACTTACGATAGGCGTTCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCCGCCAGAGACACTCCTTCTTTGTGGACGAGTTTGACAACCTCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTACAG
 CAGGACAGCAGCAGCAAGTGCTGCTTTACTAAGTACCTGACCTGTGGACCAACCCAGCTTAA
 TGGGCGACGACCGGTGCATCAAGTCTTGGGCAGGGCATGGGAAACAAATGTCTTGTATTAT
 TTCTTTTGCCATCATGCTTTTTCATATTCCAAAACCTGGAGTTACAAAGATGATCAAAACGT
 ATGAAATGAGCCAAAGGCTACATCATGTTGAGGCTGTGGAGATTTCATATTGTAACATT
 GTTTTCAAAATAAATGTTCCGAATAACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTCTGATTGAAGCTCTGTAACCCCTCAGCAAGTTTCAATTTT
 GTCATGACATGTAGGAATGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATAAAAAA
 AA
 AAG

0990172.11501

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYCTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQFVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPSGAAFOKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDII
LNAIKRVGYWGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGTCCCAGCGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTC
 TCCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTCAGAGTATAACAAAG
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTCCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCGGCCAGAATTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
 GCGGAGACTGTGAAATACCTCTACCTCCTGTTTGACCAACCAACTTCATCCACAACATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCGCTGCACTGTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTACCCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCAT**TAA**CCACTGGATAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFORVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLWVQMYKGTVSMVPVFSLEAYWPGQLSLIGDIDNAMRTFLNYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGTCTAAACTGAGTCTACCA
AATGCAGACTTTTCAACATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCTGGAGA
 AACAGTGTAATCTGTCTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT
 GGTCTGCCACTGTTCTGTGGAAATAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAAATAACCAATTACCCAGAAAGTTAATCAGTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATTAGGTTTGCGAAGGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTCAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGGCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTGTAAGTACAGAATTACAGCAAATAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHFFNRNSTILTRPGMEITKDGHLVIEEDLGPFQFEFLVAYWRREPGAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILLV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTTGTATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGTAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCGCCGCACCTACAGTGCTCTATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGAAAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTGAGTGGAGGAGGTGAGCCCCAGATCACAGCGCTC
GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATTAACCACCGCTCTCCTCCTCCACCA
CCTCATCCCCCCCACCTGTGTGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCTCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAAACAAAAATGTGTGGCAA
TAGAAGTATATCAAGCAATAATCTCCACCCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAAATAGGAGGCATTCAATGAACATTTTTTGCAATATAAACCAAAAAATAACTTGTATCAAT
AAAACTTGCAATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAAATACCTCAGGATATAAAATAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVNVASECGFTDQ
HYRALQQQLQRDLGPHHFENVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKPTWNFWKYLVPDGVVGAWDPTVSVEEVRPQITALVRKLILKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGACGGGCAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGGCGCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTACGGGGTGACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTGAGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGTCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAACCTGGAGTATGCCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATAACAACCGAGTTCCTGTCCTGCCATG
 ACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACCTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTCGCTGGGTTCGGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACACGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGAACACAGAGAACAGTCCCGTGACATTTCGGCACTT
 CCCTGAGGACACTGTGGAGCAGAAAGCGTGGGCGAGAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCCGCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCCTGCATTCCGCTGAAGGACGGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTGCACAACTACCCCTCACCAATTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTCT**TGA**ATAAAGCAGCAGGCCTGCTCGGCCGTTGGCTT
 GACTCTCTCTGTGAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATTAAGAGTCTCTGGATGGGTG
 CGGGAACTCGCCTGGGCAACAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCTGT
 TCCATCCCCACATTTCCCTGCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLET TAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEFPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCKIVGRSKDMIIRGENIYPAELEDDFFHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCAATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**ACCCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGCCCTGGATCTTCACGGGC
 TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGTGCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGCTGTGTCCAGGATGAATTCTGCATCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTGTGCCAGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTGAGGCGAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTCTGTTCCCACTGGACTGGGCTGGCCAGCCCCGTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTTGGGAAATAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTGGAGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGG
 GGTGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGCCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGQAQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPFFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

FIGURE 126

[illegible]

FIGURE 128

AAACTTGACGCC**ATGA**AGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAACGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACCCAATAAAACATTTCCATCCAAA

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTGTATATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATC
TTCATAATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGTAGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPQTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCGC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCCAGCGCAGGCGCCGACAGAGGAGTCAAGGTTCAAAATGGA
 AAGTATTTATTGACCAAAATTAAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGTTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGACGACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAACTTGTGTGATGCAGAAATACACCAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCAATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAACTGAAGT**ATAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCACTTTTAAATGTAGG
 CTCATTGCTGGAATTGTGAAATTATCAAGGCGTGATCTCTGTCACTTTATTTAAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCCTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMETPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKLFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTCTCGCCATGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCTGTCGCCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGACAGTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCAGGGCTTGATCAGCAAGACCTCCCGTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCCTGAATCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTATGCGCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAALASFILAFGTGVEFVRFTSLRPELLGGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLKQVYYHVLGLGEPLALKSP
RALRLFSLRHFPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAACCATTGCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCTGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCTGCTGCTGTCACTCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTGTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAACTGAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCACTGTCAGTGGGTTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCAGAAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAGTAGGTACTGTGGAAAATTGATGGGAGGTGAGTGTCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTTATAGTCT
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAACAAATGTAGAGTTTTATTATTG
 AACAAATGATGACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACGAACAAAATTTTACCTGTTTT
 TGGTCATTTTAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCAATTATGCATATCAGTAATCTCTTGGACITTTGTTAAAT
 ATTTTACTGTGGTAAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAAA

MASALWTVLPSRMSRLSKWSLLLLLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYIRQD
FHFRTLREHSNCSHQNPFVLVLVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQAEK
EDKMLALSLEDEHLLGYDIIRQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNLNHSKEFFTGYPLIDNYSYRGFYQKTHISYQEYFPKFVPPYCSGLGYIMSRD
LVPRIEYEMGMHVKPIKFEDVYVIGICNLLKVNIIHIPEDTNLFFLYRIHLDCVQLRRVIAHG
LSPKIIITFVQVMLRNTDCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
 GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATCAACGTCAATGATGACAACAACAA
 TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAAATGTGGCCAATGTTGACA
 ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
 AGACTCTTTCAAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
 TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
 CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
 AAAACATTGCAAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
 AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAAGTGTACTATGGATTGTGGACATTT
 CCTTCTGTGGAGACACGCTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
 CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
 TTTCTCTACTAGTTATGTTTGATTTCCTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKSGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGAATGTAAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTC AACCCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACATGGTGTAAGAAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGAAGTCGATCGAGGTCAAGAACACGATCAGG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTACAAGGAAATAAATACAAT
 CTGTTTTTTCTAAAAA AAAAAAAAAAAGT

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTATAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATNTTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAAGCAAAGGGATT
GAATCCGGATGGAACCTCCAGCCCTTTCACCCCTGGGTGGATTTTCTCC

FIGURE 143

GGACACGAGGCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTCA**ATGGC**
 GGTCTCTCGGAGTACAGCTGGTGGTGACCTGCTACTGCCACCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGCGAGTTTGTTCGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCCTGGAGTACCACTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTCCTTCTCTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC
 GGAGGAGACCTCAGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
 TTCTTGACACGAGCCGCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGTTGCTGGTGGTGTGTGCTGCTGCGGCTGGCGGTGACCCGCCCCC
 ACCTGCAGGCCTACCTGTGCTTGGCCAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGTGTCTGCCAGCCTTTTCGGCCTCTACTTCACCAGCACTTGGCA
 GGCTCC**TAG**TCGCTGCAGACCTCCTGGGGCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GGCCTTCCCTTACCCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGERSVCLTFAPFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPLILTNLCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGNTTGGAGGAGGACTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAACTTCTTACGGGGCCGATGATTATTAACGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG
 CGCTTCTGTTGCTGGCTTTGGCTTGGCTCAGTCTTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTG
 TATTACAGAATCTGTAAAGGTGCCTCCACTACGGCTTGACCAAAGATAGGAAGAGGCGCTCACAAAGATGGCTG
 TCCAGACGGCTGTGGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTGTGAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAACCTGCCTACGTGTCTCGGCAGAGACGGGCAGCCAGCAATCAGCCCCA
 GTGGACTCTGGCCGGAGCACCAGAACTAGGGCAGGCCCTTTGAGAGATCCACTATTAGGAAGCAGATCATTTAA
 AAAAAATAATCGAGCTTTGAGTGTTCTTCGAAGGACAAGAGCGGGAGTGCAGTTGCCAACCATCCGACAGG
 GCAGGGAAAATTCTGAAAACACCCTGCCCTGAAGTCTTTCCAGGTTGTACCACTGATTCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCTCGGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCC
 GGATGCTCAGAGCCCCGAGATGACAGCTTTTATGTGATTCTCAACAAAAGTAGCCCCAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCCTGGGGTTTTTATCTTCAATGTGCTGGTGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCGAGAAAG
 TGGCGCTCATCTGATTAGGCCAGTGAAAGACGTGTTCACTCGTGTGCTCCCGCAGGTTGGCGAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTTGAATGTGGATGGGGTGCAGCTGACA
 GAGGTGAGCCGAGTGAGGCAGTGGCATATTGAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAGATATTGTATTA
 CCAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATAACAATGGAACAAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACCAGCATACATGATGGAAGAATAGATGTGGTGATATTCTTCTTG
 CTGTCAATGGTGAAGTACATCAGGAATGATACATGCTTGTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTCTTGGCCTGGCACTTTTTTATAGAATCAATGATGGGTGAGAGGAAACAGAAAAA
 TCACAATAGGCTAAGAGTTGAACACTATATTTATCTTGTGAGTTTTTATATTAAAGAAAGAAATACATTGT
 AAAAAATGCGAAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAATATGATTCCAAAAAATTA
 AAACACTAGTTTTTTTTTCAAGTGGAGGATTTCTCATTACTCTACAACTGTTTATATTTTTTTCTATTCAT
 AAAAGCCCTAAAACAACTAAATGATTGTTATACCCCACTGAATCAAGCTGATTAAATTTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTTAATTACAGCTAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCTATCAACAAGAAATAATTTTTTCAAGTTAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPDEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLYGSPEAAHLIQASERRVHLVVSQRQVRQRS
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCCTTCCCAATGCCCACTAATTTTGAGATT
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV



FIGURE 150

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCCTGGGCTGTTCTGCTTGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGGAAAGTTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGTTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACCTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCAGAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
 GGGTTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**AATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCCTGTTTCGTATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCCTGGGGAAGAAA
 CTAATGTGCACAACGCGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTACAGTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAGG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAAAATAATCAGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGCTCTGAAAGAG
 AATTTTTAAATTATTAAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
 TGTCTGTAATGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVI PKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTPVSP LGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAA**ATG**GAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTG**TAA**T**T**CAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCCTCTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSYRTWQKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGOPTQHFWARL

[illegible]

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACGTGTGCACCAACACACCTTGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAATCGCCCTCCGTTTGCTCGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCCGCCG
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCGCCACCTCCACCACCTGGAGGTCCCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTGCACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTCGGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTA
 AGACATGCCCAATCTCACCCCCCTGGTGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTATG
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACT
 CAACTTGGCCCAACAATAACCTCTCTTCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGTACGCC
 TGGTGCTTCGAGACTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGGCGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGTAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTCCACGTGCTGC
 TTTGAGACACTGGGGTGACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCAGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGGCAGACACCAGTACAAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCCACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACFACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGGAACCTCTGTGACCCACAGTCACCACTATCTGAACTTATATAATTCAGACCCA
 TACCAGGACAAAGGTACAGGAACTCAAATA**TGAC**CTCCCTCCCCCAAAAACTATAAAAAT
 GCAATAGAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAAGA
 CAAAAAGTCAAAAC

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYNLGMCNIKDMPNLTPLVGLLEELEMSGNHFEIRPGSFHGLSSLLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVYTCMVTVNAGNSN
ASAYLNVSTAELENSTSNYSFFTIVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIGCFVAVTLLAAAMLIVFYKLRKRHQORS
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPINAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGGIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQMVSRETPLH
QLYSAAFSKQLQSAPTKKPALPFGDLPMPGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSPQESHITVAGWNVLADVRSFGKNDTLRSG
VVSVDLLCEEQHEDHGIPVSVTDNMFCAWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGA
 AGCTTTCTTGCCGTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCCTACAAATCCGATTACTGTGCTGTTGACTTTGTGCCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTCTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
 CAAAGGAGTTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGAAAAAAGCTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAAGTGTCTCTGTGTCTCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGGTATCTAGAAGCCCTCAAGGAAGAAAATTTGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGAGGCCAAGACGATGACCTCAGACTCAGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTTCTGGTTTGGTGCATTGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGAATCTTTGTTTGAATAAATTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAAGCTGTTACAGCTCATTTGTTGAGCTGAATTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTATCTCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAAATA
 TGCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTLC LTVVGWATS NYFVGAIQEIPKAKEFMANFHKTLILGKGKT
 LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEE VQAENPKVSRGRYRPQECKALQRV
 AILVPHRNREKHLMYLLEHLHPFLQRQQLDYG IYVIHQAEKGKFNRAKLLNVGYLEALKEEN
 WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGV TALSREQFFKVNG
 FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVG KYTMVFHTRDKGNEVNAERMKLLHQVSR
 VWR TDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGGCCGAGGAGCGACGCCGCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCGCAATG
 GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGG
 CCGGCGAGGGGTGGCCGCGAGGCTGTATGAATCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGCCAAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCGCG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGCCAGGGGCTTTGTG
 GTCTCCCATCACAGAGTTCTCGTGGGGACCTTGTGTCAACCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCCCTCCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCCTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCGCCTCGCTGAAGCTGCAGGAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAATCTCCTGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCGCTGGCCAGCAGCAGCGTACAACCTGACCCACACCTTCAGGACCTTGGGGACT
 TGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
 TGTTTGGCTTCATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGGCCACCTCTGGGGTCAAGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT
 GGAGACTCCATCTGAGTACC TGAAATTTGTTCTGTGAGAACCACGGGCTGCTCCCGCCCTCT
 ATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTCA
 TGCTGGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTCAAGCACTGCCACCAAGCC
 CCTCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCAACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCACTGCCATTCCT
 CTCATATTGGCAGCATCTGCTGTCCATTGGGGTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGACTAGAAAGAAGGTATATAAGGGTTAAAAATCCATAACTAAAGTTGTAC
 ACATAGATGGGCACCTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTAGATGATCAGCTCTGTA
 TCTGGTTAAGTCCGTTGCTGGGATGCACCTGCCTAGAGCTGAAAGGAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTGC
 GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGCGAGGACT
 AATAGTGAGTGTGACAGAGTGCTTTATAAATATACCTTATTTATCGAAACCCATCTGTG
 AAATTTTCACTGAGGAAAAGGCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCGGGCGCGG
 TGCTCACGCTGTAACTCCAGCACTTTGGAGGCCGAGCGGGTGATCAGGATCAGGAGCA
 GATCGAGACCACCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGGAATG
 GTGCGAAACCCGGAGCGGAGCTTGCACTGAGCCAGATGGCGCCACTGCACTCAGCGCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIGTFVTKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFESIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTGTCTTAGGGAGGCGAGTGCTGGCCTGGC
 CTGGATCTTCCACCA**ATG**TTCTCTGTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCAACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAAGGAGAAGAACCACCAAGCTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCCTGGAACTGCTGAGCAGAACCAATTATACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGCTGATTCCGTACTGCTTTCTGCTGCCCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGGCCTG
 CCCACACGCTCTGGTTTGGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC
 TGTTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTTGGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACAC
 AAGGACAGGAGCCGCTCCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCCGCCGCCCACTGCTGTGTCTTTCAGACTCCAGGG
 CTCCCCGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTTGGTGGTCTAAACGGATGCTGTGGGTGTTGCGACCCAGGA
 CAGATGCCTTGTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCCTGACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGGCGGCCACCG
 CTCTCCAGGAAGGCAAGCTGAGGCACGTGTGGCTGGCTTCGGCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTTGTTCGTACTCCAGGCTAACCCTGAACCTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAAATATGAGTCGGGGG
 GAATGGTGGTGAATCTTACCTCACAGGGCTGTTGTGGGGATTAAGATGCTGCGGGTGAGTGA
 AGGACACATCACGTTTCAGTGTTCAGTACAGGCCCAAAAACGGGGCACGGCAGGCTGAG
 CTCAGAGCTGCTGCACCTGGGCTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
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FIGURE 167

MFLLLPFDLSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSFGIRKLYMKSLLKIFAWATLRME
 RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSIDIIFYFCRKGME
 TIMDDEVTKRFSAAELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG
 ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
 TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
 DKSKLPILIFPEGTCINNTSVMFMKKSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
 LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
 KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCC GCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGG**GATG**GGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCCTGGGCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTA TCTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCT**TGA**AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGGA CTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 170

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAAT**ATGG**CTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGCTCTGGACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCTGTGCTCCTGTTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGAAATCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTFLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCT
GTGCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTGCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCTTGACAGACAGACAATCCTATTCCCTACCAAATGAAGATGCTGCTGCT
GCTGTGTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGCTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACACCCTTGACAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCTTGCACTTAA

FIGURE 174

MKMLLLLCGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTTGGAATTCTGGAGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

FIGURE 176

MTCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAA**TAG**TGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCCTCAGACCGGTGGCAATGTCCCCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGACCCTATGCCTTCTATAACAACCTGCCGCCGGCTCC
 AGTGTTCCTCCACAGCCCCAAAACGGAACTGGTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGGAG
 CACATCAGCCTCATGACCTTGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGGCGC
 TTCCACAGGCCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG
 CACCCTCCCCACTCAGGTTATTGATGATTTTTTCAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGGCAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCTTGACCATGTGGCTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
 TCATCGATATTATAGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCCAGGAATGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAGTGGTCCTGG
 CGTTGATGCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTCACTTTCTGACCCATCCACCTGTTTTTTGTCAGATTGTCATGAATAAAACGGTCTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
 HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
 IRFLKPWLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLEASEGS
 SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
 LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDDFFKDKAKSKTLDFIDVLLLSKDEDEG
 KALSDEDIKAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
 DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
 PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
 EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAACTAGGCCAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

FIGURE 185

GAACATTTTtagTtccCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCAtgCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTcAGTACCAGCAGCACAGCCAGGCCCTGGGGAAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAgAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

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FIGURE 186

MPSPGTVCSSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKFPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGTGTCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCTGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGA
 GACAAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCAACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGTCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGTCTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTTCATAACACAGGTTACCCTACAAACCACTGTCCCCACACAACCTTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGTTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAAGTGCTTTGACATGCCAGTGTCCTCG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAAGTGGGAGACTGGGGATGA
 CCGGTTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAAGTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTGGGGCTTTGTGGCAAAAATCCTA
 TGTTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCCTGTGGGCTCAAAGTGAAGCGCTTTGCTG
 CTGTTTCTCTGTCTGTCAAGTCTCTGGGGATGGTGGCCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATATAGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTACCAACCTTCA
 ACAGTACACCAGGATGGTGTGGAGTTCAAGTGAAGCATAGTAAAGAGCTTCAAGGAAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCTTCGGCGGCTGTCAAGTGCAGCCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCGTCTGATATCAACATGTGCTTAAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCATGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSEFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEFCLWAQTERLCCCCFLCPVRSPGDGGPHDVFSTLPSDCQLGSRRLLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGTGCAGCTTTGGCCAGATGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTCTCCATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCTATTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCTTCCCCCTGCCCGCCGTAGATTCAG
 GACATTCGCCCCGTGTGTGCCACCAAACAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
 CTCTGGGTACCCAGCAAGACGTCTGTTCCAGGCGAGTGTAGCATCTTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAA
 GGGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
 TGTGGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATCTGATTCCAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGCTGACGGAACCCAGTGTATTACCTGCTGG
 AACCAAGGAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAATCTCTAACACTGAAA

FIGURE 192

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCTGGAGCAGGAGCGACGTCA
 CCGCCATGGCAGCGCATCAAGCTTTGATTAGTTTGCTCTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGTGGCCCTTCACATATACACAAATACGGCCCTCTTGTCTATTTTTCATCCTTTCCACTTATCC
 ATACTGCATAGCAGAAGATTAGTGGATGATACAGATGCTATGATGACGCTTGAAGGAATTCGCATCTTTC
 TTACAACGGCATTGTCGTGTCAGCTTTTGGACTCCCTATTGATTGGCAGACACATCTGATTGAGTGGGA
 GCTTGTGCACCTTGTCTCACAGGAAACACAGTCTCTTGCACATATACTAGGCTTTTCTTGGTCTTTGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAATTAAGTCACTATTGTCAATGGACTTCTCTGCTATT
 GTTGGCCATTACGCACACAGGAGATGGGCGCTTAATGCTGAATGGTATAGCAAGCCTCTGGGGGATTTTA
 GGTGCTCCCTCTCACATTTTATTGAAGCATACTATTTTCACAGAGACTTGTGAGGATTAAGAGGATTTTCT
 CTTTTGAAAAGCTTGACTGATTTACACCTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTTAGGTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTTAAAATATT
 TAGCTCCATTATTACAAAAATATAAAAAAAGTTTTTCACTGAGTCAAGTACATCTTTTCTTAAAATATT
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTTAATGCCATGCCCTCCGTTAAGGGTGTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTGAAGTTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGGTGTAACAACTTTTGGATAGGTTTATTATGTTTATTATGTTAGAGTGAGTTGCAATGT
 GGGAGAAATGACATTTGAATTTCCAGTTTTTGAATCCTGTTCTATTATTAAGTGAATTTGTGATCTCCTATC
 AACCTTTCAATGTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGATATATTACATAAAA
 TAGCTTTTCAATATAGTTTAAATACACTTAGAAGTGTTTACTTACCTGGAATAATTTGCTATGCCGTACATT
 CAGAGTGGCCCTCCCTGCAAGGCCCTGCCATGATTAAACAAGTAACTGTTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTCTTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTGATTTGAGTTTATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCATTTGTTGTGTGAGTTAATGCAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAATTTCCAGTAACCAAGCATGATCAATTTATAGTGGTGGTTTACATCTAATATATATCAGGA
 CTTTTTCCAGGAGTGGGTTATAAAACATTCAGTTGGTCTGACAGTATTTTGTGAAGATATTTGTTGTATG
 TTTATCAGTATACCTTACATAAAAATTTTTCGCTCAGCAAACTCAGTAATCATGACAGCTGCTCTGTTGT
 TTTATGAAGTTTATTTTCCCTAAGTAAAGCATGACTTTTATGATATAGATGACGGACGAGACGAATATCG
 AGCCAGCTTTTATTTCCCTAAGTAAAGCATGACTTTTATGATATAGATGACGGACGAGACGAATATCG
 CGCTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTGTGGTATTATTAATGTTGAGATTTCAAGAGGAA
 GGTGACAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTCTTTGTGCTTGTGATCTACTGGAATTT
 TTTTTTCAGGAAGTCGATCTCTGCTCTTCCCTATTTCTGTTCTGGATGTCAGTGCAAGTCACTGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGTCATTGGCAGCAT
 GTGTCCTTTGACCTTGATATACTAGCTTGACATAGTGTGCTCTGATTTCAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATATGCACTGATACACATTACCATTCTTCTATGGAAAGAAAACCTTTGATGATGAACAAATA
 AGATTTTAAATATCTATTTTAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
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FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTAPH
 NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
 ITQLPNTTFRPMENLRSVDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
 LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRRNKVAIV
 VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
 LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAAQGEDVLDVAVYAFHLCEDGAETSG
 HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
 LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGTCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACCGGACTTCGACGTGCGAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGCGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGCCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGTAG
CCCCGTGCGTGTCCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGCTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTGGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRFTTRDEDLAVFLASR
AGRLLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCACTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGC
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACATATGGACAGAAG
CTGGTGGACAGTTTTTGTAACATATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP
FARDAVKKCFVCLA

00991172-111304

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCCTCCAGTCACCCCTCCCGCGTTACCCGGCGGCGC
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCGTTGCTCCAAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAATATAGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATGATATTATCTTACACTG
 AACTGATCAAGTACTTTGAATATGACTTCGAATTTATCTTGGTGCTCTTCATCTGCTGCACGTGAGTCTTTTC
 AACACCTTTTCTCTCCAACTAGACACGCAAAAGGTTCTACTAGTTTCTTTGATGGATCCGTTGGGATTAAT
 TATATTAAGTTTCCAAACGCCCAATTTTCATTATATTATGAATATGGTGTTACAGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAAACCTACCCTTAACCATTTACTTTGGTAACTGGCCCTCTTTCGACAGAAATCATGGGATGTTGC
 AAATGATATGTTTGATCCATTCGGAACAAATCTTTCTCCTTGGATCATATGAATATTATGATTCCAAGTTT
 GGGAAAGAGCGACCAATATGGATCACAAACGAGGGGAGGACATAGTGGTGGAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTATTACATGCCTTACAATGAGTCAGTTTCATTGGAAGTAG
 AGTTGCCAAATTTGTGAATGGTTTACGTCAAAGAGGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCGTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCACTGCTCTGAGGAAAGGTTAATAGAATCGACAGTACCTGGATAAAGACCCTATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACAATTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTACGCCATGGTCTGCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAACCTCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTTAAACCAGCAGAAATGACCAAGAGGGGTATACCCCTTATTTATAGGGGTC
 TCTCTTGGCAGCATTTAGTGATTGATTTTTTTGTAATTTTCAATTAAGCATTTAATTCACAGTCAAAATACCTGC
 CTTACAAGATATGCATGCTGAATAGCTCAACCATTTATACAAGCCTAAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTGGAGTTCCATAATTATGTCAGTGTAAAGGTTTCAAACTCTGGGAACAGATTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGTGATACACACACACACACACACATACACACACAGGACCAAA
 ATACTTACACCTGCARAAGAAATAAGATGTGAGAGTATGTCTCATTTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCGCTTTAATTTGGACTTGGCGCAGATAATGATATATTTAGCAACTTGCACATATGTAAGTACCTTATAT
 ATTGCACCTTTAAATTTCTCTCTGATGGTACTTTAATTTGAAATGCACTTTATGGACAGTATGCTTTATAC
 TGTATTGAAATGACAACCTTTTGCACCCATGTCACAGAATACTTGTACGCATTTCTCAAACCTGAAGGAAAT
 TCTAATAATCCGAAATATGAACATAGAATCTATCTCCATAAATGAGAGAAGAAGAGCTGATAGTGTGA
 AAATTAATATGTGATAACCTTTGAACCTTGAATTTTGAGAGATGATTTCCAAACAGCAGAAATGCAACTGCTGGGCAT
 TTTCTGCTTAAATTTCTTCCAGAGAACGTGGTTTCATTATTTTCCCTCAAAGAGAGTCAATACTGACAG
 ATTCTGCTTAAATATATTTCTTCTGTCATAAAATATTGATTTCCTGATGAGTCAGATATGCTGATTTTCA
 TAATTAATGAAGACCACTGAATATCTTTTCTCTATATAGTTGAGCAATGGGCTGAATGAAGCAACCAAGGCA
 CCATCTGCAAGTGTCTCTGTTTGTGAATTTGCTCCTTTGAAATTAATCACTAATTAATACATTAA
 AAATCAATTTGGATAAAAA

FIGURE 202

MTSKFILVSFILAALSLSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFIKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGFPVISDIDKKLGYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEER
 LIELDQYLDKDHYYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIATAVEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCCACGGGCGGGACCTTTGTAACGCGGGAGGCCAG
 GACAGGCCACCTCGCGGGCGGGAGCGCCGGGTGAGGGAGGTGAAGAAACCAAGACCG
 AGAGAGGCCAAGCCCCTTGCTTGGGTACACAGCCAAGGAGGCAGGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGGAGACGA
 CTACCATGCTTGGAAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTTCGCTGAGTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTATCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGTGGCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAAACAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFS SHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSEFTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

TGGCTCGAGCTCGAGTCGAATCGGCTCGAGGGCGAGTGGAGACCCAGAGCGGCCGCCACAT
AGCTCTGTCTGCTGCTGTACGTTCGGGCTCATCGGGAGAGCCACAGCCAGGTTCTAGCATCTTTG
 AGTGTCAAGAGGCTCCCTTCGCCGAGCTCGAAGTCCAAATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGAAATTTCTCCACTTACCGGCTCGGAGTCGGAAGCAAAAAATGTACAAGCTGGAGATAGGACCT
 TGATTTGGGCGATAGACTTTTGAAGAAATGTCTATTTCTCCAAAGTATCATGAGAAGAAGCTGA
 GGCCTGGTGTGTTTAAAGTTTGTGACAAAAAAGATATGTAGGACGATTTGACGCGAGGAGATCGA
 CAGTCCCTTCGGGGACTTTGGGATCAGAATATCTGAACACGACGAGCAAAAAATTTCTAAGAG
 CATGGATAAAAACGGCACGATGACCATGTCTGGACGAGTGGAGAGACTTACCACCTCTCC
 ACCCGCTGGAAAAACATCCCGAGATCATCCTCTACTGGAAGCATTCCACGATCTTTGATGTG
 GGTGAGAATCTAACCGCTCCGGATGAGTTCACAGTGGAGAGGACGAGGGATGTGGT
 GAGACACCTTGGTGGCAGGAGTTGGGCGAGGGCCGCTATCGACAACTCCACGGCCCCCTCG
 CAGCGCTCAAAGTGCTATGAGGCTTCATCGCTCCAGAGCAACATGGGCATCTGGT
 GGCTTTCACTCAGATGATTTGAGAGAGGAGGGGCCAGGTCATCTGGCGGGCAATGGCATCT
 CGTCTCAAAATTTGCCCGGATCAGCCATCAAAATCTGGCCTATGACAGATCAAGCGCT
 TTGTTGGTATGACGGAGGACTCTGACATTCACGAGAGGCTTTGTGGCAGGCTTTCTGGCA
 GGGGACCATCGCCACAGCAGCATTTCTCAATGGAGCTCGAAGACCGGATGGCGCTCGG
 GAAGCGCGGCGACTCAGCAGAAATGCTGGACTGCGCAGGAGATCTGGCCACGAGAGGGG
 TGGCCGCTCTTCTCAAAGGCTATGTTCTCAACAGCTGGTGGGATCAICCCCTATCGCGCAT
 GACTCTTGCACTTTATGAGAGCTATGATCAACAGCTGGCTGCAGCACTATGCATGAACACGC
 GGACCGCGCGCTGTTTGCTCTTGCCCTGGCCAACTGTCCAGTACCTTGTGGCGAGCTGG
 CCAGCTACCTGCTGCTTACTGCTCAGCCCGGATCGAGGCGCAAGCTCTATTGAGGCGGCT
 CTCAGAGGTGACATGTCAGCTCTCTTCAACATATCTCTGGCAGGAGGGGCTCTGGGCT
 GTGAGGGCTGGCGCCCACTCTATGAAGTCAATCCAGCTGTGAGGATGAGGCTACGTGCT
 TCTACGAGAACTGAAGATCACCTTGGGCTGCATCTCGCG**TGA**CGAGGCTAGGCTCGCCGG
 CGAGTGGACTCGCTGATCTTGGGCGCAGGCTGGGCTGTGCAATCATCTTCTGTAAT
 TGGCAACACTAACTGTCTCGAGCAACTGTGAAGACTGACGACCCGAGAGGAGGT
 GGGGAGAGCTGGCAGGCGCAGGCTCTGCTCTCGACCCAGCAGACACTCTGTGGTGT
 AGCGAAGACCAAGGATCTCTCTTCAGGCTCAGCAGCTCGGGCTCAGATGTGAA
 GGACAGGACATTTGCTGCTGCTCCATATGAGCTTGGAGCTGGAGCGCGGCTTAGT
 TCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGAGTGAAGTGGAGGAGGGCTACAG
 CCAACATCCCAACCTCTGCTCAATCCCAATATCATATGAAGGTGGAGTACGTGCTGGCT
 CCCGAGCTGACTTCCCAACTCAGACATGACGCCAATCTGGCTGTGAAGGAAGGAAG
 CAGTCTGGCTTGTGTTCACTGGCATTGAGCCCTGCTATGCTGGGCTCTCGGCTGCT
 TGGAGTCTGAGCTGGGCTCGGGCTCGCTGCGCTGGCTGCACAGAAGCAAGTCTGGGCTCA
 TGGTACTTCAGCTTGGCTGGACCTGTTCAGGATGGGCGCACTCAGAAGCACTCAGT
 TCCCACACTGTGGCATGAGGCGAGGTGAGCACCATTTTGAGGGCGAAGGCGAGCTTTG
 GTGTTCTGGGAGGGAAGAAAGTGTGTGGAGGCTTAATTTGACTGTTGGGAAAGGG
 TTTTGTCCAGAAGGACAAAGCCGACAAATGAGCGACTTCTGTGCTCCAGAGGAAGCAGG
 GAGCAGGAGTCTTGCTGACTGCTCAGATCTGTTCTGAGCGCTGGGGTCTCTGTCCAAC
 CCAGCAGGGGCGCAGCGGACCGACCCCACTTCACTTGTGTCTGTTCTGGAACCTATT
 ATTTTGTATTTTATTTGAACAGGATTATGCTCAACTATTTTATAGATTTGTTTAATTA
 GCTTTGTCATTTTCAAGTTATCTTTTATCATATTTATGTCTCATGTTGATTGTACTTCCC
 AAGCCCGCCAGTGGATGGGAGGAGGAGAGAGGGGGGCCCTTGGCGCTGCACTGCAT
 CTGCTCCAGAGAAATTTCTTTTGGGACTGGAGCGAGAAAGCGGCACGAAGGCAGACGGCT
 GCTCCTTTCTTTTGGCAGGTTGGGAAGGGCTTCCCCAGCCTTAGGATTTCAAGGTTTGA
 CTGGGGGCTGGAGGAGGAGGAGGAACCTCAATTAACCTTGAAGTGGAACTCAGTTATTTC
 CTGGCTCGGAGGTTCTTTTATTTCACTCTTTTCTGAATCTCAAGGCACTGAGGTGCCCT
 CACTCTGAATTTTGTGGTGGGGGGGCTGGAGGAGAGGTTGGGGGCTGGCTCGCTCTCT
 CAGCCTTCTGCTGCTTGTCTTAACTATGCGCGCAACTGGCAGCTCAGGTTGCATCTCC
 ATTCACACAGATGACCTGATGAGGAATCTTCAATGAGATGCAAGATCAATGCAAAAT
 GTTATATTAAGACATAAATCGGAGTCGTCAAAAGCAAAATTAAGAAAGATTTGACGCTAG
 AAGTTGTCATTTAAAGCAGCTTCTTAATAAGTTGTTTCAAAGCTGAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAISISVYVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCT
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTC
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCACAGTGGTCTGGGATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCGAGAATGTGACCA
 TGAAGGTTGTGTCTGTCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGCGGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTCTCTCTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAATCTTTCACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTACACAAGTGTTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGTCTCTGAGGAAGCCCCTGGAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLNSKASLCVSSFFAISWALLPLSPYMLK

FIGURE 209

[illegible]

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGLLYYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGAAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATTATG
 AATCTAATGGAATTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCACTAACGCCACCTGTCAGTTCCTGTCTGGTGAAACAAGACTCTTGGAGGAGTCA
 TCTTTGAAAAGTTTGTAGTGTGCAAAATGTAACAGCTTAACCCCCACGCTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAAGGTCTGGGGCTGCACCTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCTTATTATTA
 AAGCACTGGTTCATTCTACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTCTGCTGAATCTGGGTCCCCGGGCGCGGGGGCCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCCATGACCCGCAG
 CTACCGGAGCACGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACCTATCAACAATGT
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTCACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAATCTCAACCTCT
 CTGCCCCTTCAATCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGAAAA
 CAAA

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FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINeedGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMFWGEPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTFPPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVFTMQPIDRNQR

FIGURE 215

CCCGGGTCGACCCACGGCTCCGGGGAGAAAGGATGCGCGCCTGGCGCGCGGTTGGTCTGCTAGCTGGGGCA
 GCGGCCGCTGGCGAGCGGGCTCCAGGGCGACCGTGAAGCCGGTGTACCGCGACTGCGTACTGCAGTGCCGAAGAGCA
 GAACCTGCTCTGGGGGGCGCTCTGAATCACTTCGCGTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGAGCACTGTAAATATGAGTGTATGTGGGTACCGTTCGGGCTCTACCTCCAGGAAGGTACAAAGTGGCT
 CAGTTCOCATGGCAAGTGGCCCTTCCCGGTTCTTCTTCAAGAGCCGGCACTGGCCCGTGGCCTCGTGTCT
 CAATGGCCTGGCCAGCCTGGTGAGTCTCTGCGCTCCACTGTCTACCTACACTCAATCTACCTGTGCTGCGTCAAGAC
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTCTGTGTCACACTCTTCCACACCAAGGACACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCTCCACTGTCTACCTACACTCAATCTACCTGTGCTGCGTCAAGAC
 CGTGGGGCTGCAGACCCAGCTGTGGTCACTGCTTCGGGGCTCTCCTGCTGCTCATGCTGACCTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGCTATTGGCCTGGTCAACCTG
 GTGTGTGGCTGGCCTGGTGCCTGTGGAACCCGCGCGCTGCCTCACGTGCGCAAGTGGTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
 TCTGGCACATCAGACCATCCCTGTCCACGCTCTCTTTTCAGCTTCTGGGAAGTACAGCGCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAAGCTGGACTGAGAGACCTTGGAGCGAGTCTGCCCAAGTGGGGATCCTGCCCC
 GCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAAGTATTTCTCTTTTCAACTTCTTGAACCTTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGCCCTCACACGCTTGGAGTCTGTTCTAGGG
 AAGCCCTCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCCTGGAGTGAACCTGGGTGGAAGTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCCACACGCTCTCTCCACATCCCAAGCTG
 CTTGGTGGGTCTTGAAGCCCTCTGTCTACCTGGGAGACAGGGACACAGGCTTAGGGATACAGGGGGTCCC
 CTCTCTTACCAACCCCACTCTCTCCAGGACACCACTAGGTGGTGGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACCGGCAATCTCCCCATGGGATCTTGAGGGACCAAGCTGTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTCCCTCCAGCAAGTCCCAAGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAAGGGCA
 AGGATCCTGTGCTGCTGTCTGGTGTAGAGCTGCCACGCTGTCTGGGAGTGTGGCCAGGCTGAGTGCAATAGG
 TGACAGGGCCGTGAGCATGGGCTTCAAAGTGTGTGTGTGAGGGGGTGGGTGTCTAGCGTGGGTAGGGGACGTGTG
 TGGCGCTGTGTGGGATCTGAGATGAGTGAAGTGCAGGCTGCGGTGAATGTGCCAAGTGAAGAGTTGGAGCAGGAT
 GAGGGAATCCTGTACCATCAATCACTTGTGAGGCGCAGCTCTGCCAAGAGCCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCTGTGTGATGTTCCCTGTCTGTGGCCCTTTGCCCGCTCTGTGCAAC
 CTCACAGGGTCCCAACACACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAAGGAAATGGGGATGGC
 TGGGGCTCTCTCCATCTCTCTTTCTCTCTGCTTCGCTTCGATGGCTGGCTTCCCTCCAAACCTCCATCCCCCT
 GCTGCCAGCCCTTTGCCATAGCCTGATTTGGGGAGGAGGAGGGGCGATTGAGCGAGAAGGGAGCAAGCT
 TATGGCTGGGTCTGGTTTCTTCCCTCCAGAGGGTCTTACTGTTCAGGGTGGCCCGAGGCAGGCAAGGGCC
 ACATATGCTGTGCCCTGGTAAAGGTGACCCTGTCATTTACAGCAGCCTGGCATGTCTCTGCCCAAGG
 AATAGAATGGAGGAGCTCCAGAACTTTCCATCCCAAGGAGCTCTCCGTGTTGAAGCAGACTGGATTTTG
 CTCTGCCCTGACCCCTTTGCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCGACTCAGGAGCTTCGGGTG
 GCCTGCGCTAGCTTCTTTGATACTGAAACTTTTAAAGTGGGAGGGTGGCAAGGAGTGTCTTAATAAATCA
 TTCCAAGCCTCAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFEHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWVWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPKESSSTKETERTKETKAEDEL
DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVYHQMDNAQDLLSFQGLQVINGLNSTEPLVKEYAAF
VLGAAFSSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGLQVLRRLVQEKGTAVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELGVSNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

[illegible]

MGAAVFVGCTFVAFGPPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVWVFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPPYFLTSAFLTAAIILLHTFGWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFNLNPWEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTGGGGAGTTGTGTTTTTGGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCCTGTCCTGGTCAGGCCCCACCCCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTCGGCCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCGTCTCTGGTCAGGCCCCACCCCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGTGTCCCAGAGCCCAGGAGGAGCGAG
 TGCCACAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGTGCT
 AGACTCCTATCTTCTGAATTCATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCAGACCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCGACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACGAACAGAAGAATTCGTCCCACTAAAGATGTAGACCCAT
 CAACGTCTCCTCTCATTTGCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGAAGTCTGCTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCT**TGA**GTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTTCAG
 ACCCTCATTTCTTCCAGAGATGTTGAGAATGTTTCATCTCTCAGCCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTTG
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAA

FIGURE 226

MATARPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAACRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPASAGTKCL
VSGWGTTKSPQVHFPPKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDGGP
VVCNGLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGTGTCACGACCGGTGGAAGACCATGGCGGCGCTGCCAACTTGAGGACCGCGCGCGCA
 CAAGCCGACGCGCGGAGCTGCGGGCTACGTGCTGTGCACCGTGTCTGCGCCCTGGCTGTGTC
 TGCTGGCTGTAGCTGTACCCGGTGCCGTGCTCTTCTGAACCAAGCCACGCGCGCGGCGCAGC
 GCGCCCCACCTGTGCTCAGCACTGGGGCTGCCAGCGCCAAAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACGCTCCGACCTCAGCATCCTCATTGACCCGCGCTGCCCGGACCTCACCAGACA
 GCTTCGCACGCGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCG
 CAGCCACGGCTGGTGGGACCAAGGACAGGAGCAGAGCTGCTGGACACGCTGGCGGACAGCTGCC
 CCGGCTGCTGCGCCGAGCCTCAGAGCTGCAGACGGAGTGCACTGGGGCTCGGGAAGGGGCATG
 GCACGCTGGGCGAGGCGCTCAGCGCCCTGCAGAGTGAGCAGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACGCGACATCCTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGCGCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCC
 GGGGAACCGCGCCCGGGGCTGTGCCACTGCTCCCGGCCCCGAGACTGTCTGGACGTCCCTC
 CTAAGCGGACAGCAGGACGATGGCGCTACTCTGTCTTCCACCCACTACCCCGCGCGGCTT
 CCGGTTGTAAGTGTGACATGCGCAGGACGGCGCGGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTTCTTCGGGGCTGGGACGCGTACCGAGACGGCTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCGCTGACCAACAGGCTGCCCTACAGGCT
 GCACGTGGACCTGGAGACTTTGAGAATGGCAGCGCTATGCCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCGTGGACTCCCTGAGGAAGACGGGTACCGGCTCACCGTGGCTGACTATTCC
 GCGACTGCAGGCGACTCCCTCCTGAAGCACAGCGCATAGGTTTACCACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACTGTGCCGCTTCTACCGCGGTGCCCTGGTGGTACCGCAACT
 GCGACACTCCAACTCAATGGGCAGTACCTGCGGGGTGCCACGCGCTCCTATGCCGACGGC
 GTGAGTGGTCTCTCTGGACGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 CCGGTCGCGGAGGACCG**TAG**ACTGGTGACCTTGTCTTGGCCCTGCTGCTCCCTGTCCG
 CCCACTCCGAGCCCACTTCACTCTTTCGTGAATGTTCTCCACCCACTTGTGCCCTGGCGGAC
 CACACTCTCAGTAGGAGGGGCGGGCCATCCCTGACACGAAGCTCCTGGCGCGGTGAAGT
 CCACATCGCCTTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGGCTC
 TGTGTAAGGGGCTGGCAAATTTGACGACCCCACTCCTGCCCTGCCCGCTGTGACTCCGG
 TGCTGTTTGGCTCCCTGGCAGGATGGTGGAGTCTGCCCGAGGACCCCTTGCCTGCCCTGCC
 GCGCAAAATCCGGCAATTATGGGACAGAGAGCAGGGGGCAGACAGCCCTGGAGTCTCTC
 CTACAGCATCTGTGGGAATCTCAGGTCTCTCTGAGGTCAAGGTCTGAGGCCAGTATCCTCCAG
 CCTCCCAATGCCAACCCGACCCCGTTTCCCTGGTGCCCAAGAGAACCCAGCTCTCCCCAA
 GGGCTCTCAGCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTCAAGGATGGG
 GAGCTGCTGCTTTGGGGACCCACGCTCCAAGGCTGAGACCAAGTTCCCTGGAGGCCACCCAC
 CCTGTGCCCGGCGAGGCTGGGGTCTGCAGTCCCTTTACTGCTGTGCCACCTGCTCTCTG
 TCTCAAATGAGGCGCCAACCCATCCCCACCAAGCTCCCGGCTCCTCCTACTGGGGCAGC
 CGGGGCTGCCATCCCAATTTCTCTGCCCTTGGAAAGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGGCTAATGGGAAGCTCTGGTTTTCTGGGCTGGGGCTGAGCAGGCTGGGATGAG
 GCTTGTACAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCTCCAGGCTCCAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCCCTTGCC
 ATTGACCGCTGGCCACTTGGACCCAGGCCAGGCGCGCGCGCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGCAATGGGGTGGGGGGACTGGGGCACCAGACAGGCCACCACTTGGGACA
 CTTTCTTGTGTAATCTCCCAACCCAGCAGCGTGTCTATCCCACTCCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGCGAGCTCCAGGACAGCAGCACAAGGCGAGGCTGGAGCGCGGG
 TCCCTCAGCTGTCTGCTCAGCAGCCCTGACACCGCGTGCCTTACGTACGGCCAGATGACAGG
 CGGCTTTTCCAAAGGCTCCTGATGGGGGCTCCGAAAGGCTGGAGTCAGCTTGGGAGCT
 CGCTAGCAGCTCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GGTCCTTAGGGGTGGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAAATAATTTGACTTGGGACCACTGGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCAGTGCCACCAGGTCATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLRARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCILDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSGFVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMIRPVREDR

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FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCT
 TGCTTCCCTGAAGTACAGTACAGTACGCCGCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCTGCATTCTCAAGCCTCTGCCCAACTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGAC
 TTTGCTGTTGGTGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGAGGAAGTCTGCAGCATGTGGC
 TGA AAAACTCTGTCGTGAGCTGTATAACAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAGAAGA
 CCTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCCTGGCTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGACTGCAAGAATGGAAGCGTTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAATGGGTTCTCGTG
 TTTCTGTTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTCTCAATGCTCAATATCACCTCCCTGTTTTCAT
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCCAGATTGTACC
 AGCAATACACAAGGAATCTTTTTGTTTGTTCAGTTTCTACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCCTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCATTAAGACTCTGATAATG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCTATATCAG
 AACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAAGTCTCTATTTTCTTCCATTGACCCATATTTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNICYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPPTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGECD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

CGCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCGCCCGCGGGG
 CCGGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTCGCCGGGGCCGGGAGCCCGGGTCCGGGCGCC**ATC**CGGGGCATCGCTGCTGCTG
 TCGGTGCTCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCGTGAGCCT
 GCTCAGGCTACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCGCGCGGCAACACCAACGCGGCGCGGCCGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAAGCCCGGGGCCGCGCAAGCGCCGGGAGAAATTGGGAGCCGCGCTCTGGCC
 CTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTACGAGACCCTACATCAGCA
 CGGAGCTGGGCGATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCCTGTGGTGTCTCCTGAC
 GGGCGCACGGGGCCGCCGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTGGTGCTGACACCACTACACCGAGGCGCACGGCCTGGCACGCCTAACCTGG
 CCACCTGACGCTGGCCTCCGCCGCCACCTGTACTGGGGCGGCCAGGACTTATCGGCG
 GAGAGCCACCCCGCCCGCTACTGCCACGGAGGCTTTGGGGTCTGCTGTGCGCGCATGCTG
 CTGCAACAACTTGGCGCCCACTGGAAGGCTGCCGAACGACATGCTGAGTGGCGGCCCTGA
 CGAGTGCTGGGTGCTGCATTCTCGATGCCACCGGGGTGGGTGCATGGTGACCACGAGG
 GGGTGCACTATGCCATCTGGAGCTGAGCCCTGGGAGGCCAGTGACAGGAGGGGACCCAT
 TTCCGAAGTGCCTGACAGCCCAACCTGTGCGTGACCTGTGCATGTACCACTGACACAA
 AGCTTTGCCCGGAGCTGAACCTGGAACGCAGCTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCAGAATACACGACCTATGGCCGTTGATGGGAGCCGGGACGCTTGGCCCTGGGTGATT
 CCAGCACCATCCCGCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCCTGCGCCGATGGCTCACCCCGCTGCCACTGGCTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTTACACCCGGCCCTTG
 CGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGAGCCTTTGATCCGGCCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCCCGGCCCTCACTC
 GCCGAGTGACGCTGCTCCGCCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCACAGTCTCACTGTGCTGCTGCTAGCTGCGGCTGAGCGTGACCTGGCCCTTG
 CTTCTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCATGCAGATGTCTTCGACCT
 GTCAAGGCCACAGTGGCAGAGCTGGAGCGCGCTTCCCGGTCGCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGACCTCACCACTGCGCCTCATGGATCTACTCTCAAGAAGCACCCG
 TGGACACACTGTCTGCTGGCCGGGCCAGACACGGTGCTCACGCTGACTTCTTGAACCCG
 TGCCGATGATGCCATCTCCGGCTGGCAGGCTTCTTTCCATGCATTTCGAAGCTTTCCA
 CCGAGTGTGGCCCCACCAAGGGCCTGGGCCCCAGAGCTGGGCCCTGTGACATGGCCGCT
 TTGATCGCCAGCGCCAGCGAGGCTGCTTCTCAACTCCGACTACGTGGCAGCCGCTGGG
 CGCCTGGCGGAGCCTCAGAACAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGCCAGAGCTGACGCGGAGGCTCAGTGAGGACCTGTACCCAGCTGCTTCCAGAGG
 GTGCTTTGAGGCGCTCGGCTCCCGAACCCAGCTGGCCATGTACTCTTTGAACAGGAGCAGG
 CAACAGCACT**TGA**CCCCACCTGTCCCCGTGGGCCGTGGCATGGGACACCCCACTTCT
 CTCCCCAAACACAGAGCCACCTGCCAGCCTCGCTGGGCAAGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCACTGGTCCCTCTCTGGCTCTGGGTCCCTGGGCTCTGGACACGACTGGG
 GGAGCTGCCCCAGAGCCACCACTTCTCATCCAAACCAAGTTTCCCTGCCCCCTGACGCT
 GCTGATTGGGCTGTGGCTCCACGTATTATGACATACAGCTGCTGACGCGCAGCCCTGC
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGGAGGG
 GCACTCTCCCAACTCTCCCTTTTGGACCTTCCGAAGCTCCTTGCCCTTAATAAAGCTGGCCA
 AGTGTGGAAGAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVTRYISTELGIRQRLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERP IGHHLALRHLE
QHGDDEFWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDDEWLGRCIIDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFERSALTAHPVRDPVHMYQLHKAFARAELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTALTEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPOGGRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGGPPPELGRDTGRFDQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSHLVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEONGST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCACTGGGCGAGGGAAGTGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTACCGATTTCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCPAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGAAGAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTT
 TTCCCCGCCCCTGAGACCCTGCAGCACCATCTGTCA**ATG**GCGGCTGGGCTGTTTGTTTGAAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGCTTCTT
 CTTTGGCGTCTCCATCATCTGCTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTAATACCGAGAGGCCAATGGC
 CTTCCTCATGGAATCCAATGCTTCGACCCCGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPDSHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE



GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTTGGCGGCAGCGGCACGCGAGGGC
TCCGGGCGCGCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGCGGGGAAGCGGCCCCAGAACCGACACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATCCAGGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CGGCTTGCTCTGCTCGTCTGTTGCTCTGCGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCCGACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCGACGCGTGGGATTGCGAGCTTCAGCGGGAAGGAGTG
 TCCCATACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCTATTACACAAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACAGAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCGCGGGAGGTGGTCTGCACCGAAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCACTTGTATTGTATGCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCTCCTTAGGCAC
 CGGAAGACCTATGCCATCTATGACTGTCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCAGAGAATGAGGCCCCCAGTGGCCCTTCCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGTGCAACCCACCTCCTGGAGATGCTGATTCACTGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGCCCAAGCGGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**GA**ATT
 CTTGCCCCCTTCAAGCAGCTGCAGCTGCCGTTTCTCTCTGCGGAGGGGAGCCCAAGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTTGAATTA
 CTTAGAAATTCATTTCTCACTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGATTGGACAGCAGAAAAAGATTTCATCACACACAGAAAGCTC
 GGCTGGCAGCACTGGCCAAGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTL SVVFD AFITG
QGKKDWSLFRMFRTLT EPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLDDTAMINNSRNLNIQLKWKRP PENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVS IQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLNLPTPDFSMPYNVICLTCTVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTCCCCAAAAGAGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEgGNKDEDVSRPYFEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAGGGTGTGCACCTTCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGAGCCACCACC**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTTGAGCCAAAG
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTCTCTTGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAGCCTTCAGGCATCAACGCACAGAGAACATTAAAGAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCAAGGCCCAACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGAGCAGCCAAAGGAAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGAGG
 GTGTCAAGAAGCACAGGGCAAAGCGGCAACCAAGCCAAAGACGCTCATCCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCACTCCACCTAAGGAGAAGAAACCTCAGGCCACCCCACTCCCTTCCCTTTCCAG
 AGCCCCACGAGCAGAGAAAACCAAGACTGAAGGCCGCGCAACTTCAAACTCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCAAGCTCGCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGCAACACTTTGACCAACC
 CTTTGGCTTCATGGAGTCAACTACTCCTTGGTGCAAGGTCGTGACACGCTTCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCATCACCTGT
 GCCGTGGTGGGCAACGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCTTGGAGGCAC
 CCGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTGGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGTGCTCACTGCCCCCT
 AGCTCTGTGACACAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACAGCGTCCCTGGTC
 CCGGAACCTGCCAAAGCCAAGAACT**CGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGAACTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTCTGAAGTCTTTCAGTACATTGCTGAGGTCCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCACAATTCCTGTCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGATTTACTTAACCTTCACTAC
 AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGCTCTATACCTTGTCTTG
 TCTTTAAGCTATTTGACAACCTTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPA PENNALNTQTQPKAHTTGD RGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQGNQGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLENLTLFLDSRHF
 NQSEWDRLEHFAPPPGFMELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVVKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CG**ATG**CGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCGG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAAACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAG**TGA**GCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCTCGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCCACC**ATG**CCACCCGCGGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTCGGGGTGGCAGGAGTCTTCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTACGAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILEVAVVATTICCFLLSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

CGGGAGAGCTAGGCCGCGGGCAGTGGTGGTGGCGGCGCAAGGTTGAGGGCGGCCCGGACG
CCCCAGGTAGGTGATGACCAAGAGATGCTGGTGTTCGCCCTCAAACTGGGTCCTTGCAACATGT
TCATTTTCTACTTTCTACCTGTTGGCTCTTTAACTGTGTCCACTCTTTCATGGTGTICAGAG
CTGTGAAGCATCTCCAAAGACGTAGTGATGGACACCAATTTCTTGGAAATAAAATACGATTC
CCTAGTACGTCATCCAGGTTCTATTATGATCTCTTGATCCATGCAATTTGATACAGCATGCA
CTCTTGGGAGACCGAAAGATGAAATATCAGCCGACAGCCGACACCACTATGCTGCA
TAGTCAACCACTGCAAGATATCTTAGGGCCACCTCAGGAAGGAGCTGGAGAGAGGGCTATCGG
AAGAAGCCCTCGACGTCCTTGGAAACCCCGCTCAGGAGCAAAATGCACTGCTGCTTCCGGA
CCCCCTCTTGTGCGGCTCCCGTACACAGTGTGTCTTACTATGTGGCAATCTTTGCGGAAT
TTTCCACGGATTTTACAAAGACACTACAGAACCAAGGAAGGGAACTGAGGATATAGCA
CAACACAAATTTGAACCCCTCGAGCTAGAAATGGCTTTCCCTCTTTGATGAACCTGCCCTT
AAGACAGTTTCTCAATCAAAATAGAGAGAGCCAGCCAGGCATCTAGCATCTCCAATATGCC
ATTGGTGAATCTGTAGCTGTGTGCAAGGACTATAGAAAGCACTTTTGATGTCACTGTGA
AGATGAGCAGCTATCTTGGTGGCCTCATCATTTTCAGATTTTGAGTGTGTGCAGGAAGTAAC
AAGAGTGGAGTCAAGGTTTCTTTTATGTGTGTGCAGAGACAGATAAATCAAGCAGATTATGC
ACTGGATGCTGTGGCTGATCTCTCAAAATTTATGAGGATTTATTCAGACACAGATTTCCCT
TACCAAAACAGAGATGTGCTGCTATCTCGAATTTCACTGCTGGTGTGATCGAAAGCTGGGA
CTGACACATATAGAAATCTCTCTGTTGTTGATGACGAAAGCTCTGCAACAGTGTGA
GTGTCGCTACAGAGAACTGCTGGATGAACCTGCGCAAGCTTTGGGAAGTTGGA
TATGCAATGTGGAAATGATCTTTGGCTAAAGAGGATTTGCCCAATTTGAGAGTTTGTG
TTGTGTAGTGTGCGCTTCTTAATCTCTACACAGTGGAGATTATTTTGGCAAGTTTGA
CCGTGAGGTGTAGTGTGTTGATGATTTCTCATGTATGTGTGCTACACCTTGGAAATCTG
CTCAAGTGTGATGTTTGTATGATTTTCTCATGTATGATTTGATATTTGATATTTGATAT
CTAGSGAGTATCTTAGCGCTGACGATTTAAAGTGGTGTTCAGACGTATCTCCAGAGCA
TATGTTAAAAATACAAAAGAGGACCTCTGGGATATGTGCAAGTATTTGCCCTACAG
ATGGTTGAAGAGGATGGATGGCTTTTGCCTGAGAGTCAACATTCATCTCATCTCAZ
ATGCTCAGGAAGGGGTGGATGTGCTGAGGAGCAATGAACACTTGGACACTGCAAGGGGTTT
TCCCTTAATACCATTCAGATGAGGGGAGGATTCACATTAAGCAACAGACACTACATGA
AGGGCTCTCAGGGCCGCGGACACTGGGTACCTGTGGCATTTGCCATTCGACTATCATCC
AGCAATCCCAACTGTCTCATCATGATTTTGCCTAAAAACAAAACAGATGTGCTCATCTCC
AGAGATGGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGCTATCG
AATGATCGGGCAAGTCTCTATAACATGCATTTCACTGCTCGAGCATTTGGGAAGTCTCCAT
TGAAAGGGCTTTGGATTTTCCCTGTACTTGAACATGAAACTGAAATATGCCGCTGTTC
AAGTCTTAATGAGCTGATTTCTTATCTATAAGTTAATGGGAAAAGAGATTAATGAAGT
GAACTCAATTCAAGGCTTTCTTCACTCAGGCTGCTAAGGGACCTGATGATAGCAGACT
GACAGCAGGGGCTCAGTCTCAGAGCAAACTGCTGGGAGTGAACTACTACTCTCGCTGT
TGCACAACTATCAGCCGTGCTCAGAGGGCAGAAAGGCTATTTCAGAAAGTGGAAAGAACTC
AATGGAAATCTGAGCTGCTCTGACAGTGACCTTGGCAGTGTTCGTGTGGGGGCCAGAG
CACAGAAGGCTGGGATTTTCTTATAGTAATATCAGTTTCTTTGTCAGATCTGAGAAAG
CGAAATTTGAATTTGCCCTCTGCAAGACCAAAATAGGAAAAGCTTCAATGGCTACTAGT
GAAAGCTTTAAGGAGATATAATGAAAACCTCAGAGTTTCCACAATTTTCACTCATGAT
CAGGAACCCAGTAGGATACCCCTGGCTGGCAATTTCTGAGGAAAACCTGGAACAAACTT
TACAAAAGTTTGAATTTGCTCATCTTCTCAATGCCCACTGTAATGGGTACACAAATCAA
TTCTCCAGCAAGAACACGGCTGAAGAGGTTAAAGAGTTCTTCAGATTTTGAAGAAAGTTG
TTTTCAGCTCGGTTGTGTCCAACAGCAAAATGAAACATTAAGAAACATCGGTTGATGG
ATAAGAAATTTTGAATAAATCAGAGTGTGGCTGCAAAAGTGAAGAGTGTGAACGTATCTAA
TTCTCCCTCTGCCCGGTTCTGTATTCTCTAATCAACAACTTTTGTGAGTGTATTTCAA
ACTAGAGTATGGCTGTTTGGCTTCCAATCGAGATGAATTTTCCCTTCCAATCATTTTGA
CTATCCCTGTGAAAAGAAATGGCTGTAGTTTTCATGAATGGGCTTTTCATGAATGGGCTA
TCGCTACCATGTGTTTGTTCATCAGAGTGTGCCCTGCAACTAAACCCAGTGTGGGT
TCCCTGCCAGAGAAATAAGTACCTTATTCTCTCAAAAATAAAAAAATAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLIIHANLTTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQVLE
 HPPQEQIALLAPEPLLVLGYTVVIHYAGNLSETHGFKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSLYLVA
 FIISDFESVSKITKSGVKSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHLELAHQWFGNLVTMEWWNDL
 WLNIEGFAKFMEFVSVSVTHPELVKVDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFEQGLNELIP
 MYKLEKMRDMNEVETQKFAFLIRLLRDLIDKQTTWTDGSGVSEQMLRSELALLACVHNYQPCV
 QRAEYFRWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTKSQIEFALC
 RTQNKEKLQWLLEDSEFKGDKIKTQEFQILTLIGRNPVGYPALWQFLRKNWNKLQKFELGS
 SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTIETIENIGWMDKNFNDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteinases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCACTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGCCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTGGGGCTCAAATTTCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
 GTGCTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAGGGCTGCGTGGGCCAACCTTCCAGCTTCTTGTTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGTGAGGGCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCCTTCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTCATATCTACTCACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGGAAGTGGCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
 PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
 LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
 LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
 SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
 VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES�TWGVGLALAPALWWGVVC
 PSC

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
 PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
 LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
 LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
 SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
 VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES�TWGVGLALAPALWWGVVC
 PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATGA**GGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTGTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGTAT
 GGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCCAGCTGTCTGCCAGGGCCGCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGCAAGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTGTCTAAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAAATG
 AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAAGC
 TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAATAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G F N G E P G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGAGCAGGCAGCGGTCTTAGCCAGTTCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCTTGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
TTTTAAGACTCTCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT
CCTACATTAATAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTTEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCTGGGTGGTGTATCCCCCTTGGGGC
 TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTAGAGGAG
 CTGCTCAGCAAATACCAGCACACAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGTTCGGGGCCAGGTGCAGCCTCAGGCCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGTGGGGC
 CTGGGCCACCGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCTGTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTGGGGTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCACCTTGGAGAGTCTCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGTCAACCTTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCTCTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCTCTCTGTCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAAACATGGTAAAGCCCCGCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAAA

FIGURE 256

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLEELL SKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR
GGSRLCSVLFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTCTGATGTGGGGTTCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
CTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTATAAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
GAGAAGAGCCACAGCATAAAGACATGCCCTGCTTGGTGGTTCGAGGAGATGGTGGCCCTT
CGAGAGCTTCTGATCTGCTGGTTCGTGCTTCTGACGTTTTCTGCCCCGGCCGAGGTGATC
CCAGGACAGCCATGTGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGACAGGGCTGG
AAAAATGTACCAAGCAACAGGCGATACATCTCAAGAATTTCAAGAGTCTCAAAAATATATA
TCTGTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAATCAAGAGTGCAGTGGGTAACTT
GGCATCGAGAGTTGAACGTGCCCAACGGGAGATGACTACATACAATACCTTCGAGAGGCT
ACAGGTGCATCGTATCAGAGACAAGACATGGCAGAAATGTTGCTCCAAGAAGCTGAAGA
GAGAAAAGATCCGGCATCTGCTGAATGCAAGTGTGACAACTGCTGATGGCCATAAAGTCT
TTTGAATAATGTAAGAAGATGATGGACACATGGCTCTTGATGAAGAAGATGCTGTCTATA
ACTCTCCAAAGGTGTACTATTAAATTTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAC
ATACGGGCACTTATGSGAGATAACACAGCCAGCTCCCGGAGGCAAACTCTAACACTTTC
CTGGCAGGGAACAGGCCAAGTGATCTCAAAGGTTTTCTATTTTTTTCAATACCAACCAACT
CTAATGAGATAATCAAGATTAACCTGCAGAAAGGAGACTGTGGAAGTCAAGTGTCTGCCCA
GGAGGGGTAGGCCAGGATTTGGTTTACCAGCATCCCCCTCAACTTACATTGACCTGGCTGT
GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATCATAGCCATTGGTGTCTCA
CAAGAGTTAGCGCGGCACACTGGGAGTGAGCATTCATGGGATACCCCATGCGAGAAGCCAG
GATGCTGAAGCCCTCATTTCTCTGTGTGGGGTTCTCTATGTGTCTACAGTATGGGGGCCA
GGGCCCTCATCGCATCACTGCATCTATGATTTCTACTGGGCATATCAGTGAGGAGGACATTCG
CCAACTTGTTCTTCCCAAGAGACCAAGAAGTCACTCATGTATTCATTACACCCCAAGAGAT
AAGCAGCTCTATGCGTGAATGAAGGAAACACGATCACTTACAACCTCCAGACAAGAGAAA
GCTCGCTCTGAAGCTAAATGTCATTACAGCTGTGAGAAGAGCATCTGGCTTTGGCAGCTGTTC
TAGCAGGACAGTGAGGCTATAGCCCTTACAATATAGTATCCCTCTAATCACACAGGAAAG
AGTGTGTAGAAGTGAAGATAGTATGCTCTCTTTCCAAATGTACCTGCTTATGATATCTTC
CAAGAGCTTATAGTAGAGCATATCATCAGGAAGATTTCAACAATCTGCTCATTCATCCCCAAA
CCTCTCGCTCTCAAGGATGACCATTTGTATACAGGCTACITGAGCCCTTTTGGTTTACT
GCTCCCCAGCATTTACTGTAACCTTGCCATCTCCCTCCCAACATTAGAGTTGATGTGCCAGC
CCCTAATATTCACCACCTGGCTTTCTCTCCCTGGCCTTGTGTAAGCTCTTCCCTTTCT
CAAAATGCTATTGATATCTCCCACTTTCTACTGCCCACTAAAATAGCTATTAATATTCTTT
CTTTTCTTTTCTTTTCTTTGAGACAAGGCTTCACTATGTTGCCAGGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCTTCTCGCTCAGGCTCCCTAAGTACCTGGGATACAGGCATGGCCAC
CACACTGGCTTAAATATCACTATTCTTATGAGGTTTAACTCTTATTTCCCTAGCCCTGTCT
CTTCACTAAGCTTGGTAGATGTAAATAAAGTGAAATATTAACATTTGAATATGCTTTT
CCAGGTGTGGAGTGTGTCACATCATTTGAATTCGTGTTTCACTTTGTGTAACATGCACAG
TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAAACAACATTAACAAGTGAAGATACAGC
TAGAAAACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAGCATCAATACGTATTTCT
TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCTCAAAAATAAGTCTGTCCC
TTTAGACGTTTTCATGTCTGCACAGCAAGCTTTCATAAGCGCTTCAATAGTAAATTTCTCC
AGAAAACCAAGTCTAAGGTTGAGGACCCCACTTAGCCCTCTGCTTGTCTGTCTGTCTCTGT
TCTCTCTTTCTGCTGTTTAAATTCAAATAAAGTGACATGAGCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKEKKIRTLNASCNMLMGIKSLKIVKKMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGCGAGCTCATGGGGCTGTGGTGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGC
 GTAGCGCGGGGGTGGCTGCGCGCGGGGAGGAGGAGCGGGCCGGCCCGCTGCCAAAAAGC
 AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACAACAACCTTCAACCCACCGCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCACGGGGACACCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAGGCGCTGTCA
 TCGACATTGGCATTGTCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCAACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCAGGAGGTTGGTGCAGCCCTCGAA
 CTAAAGGGCACTCCGCGGCTGTGCATCGTTTGTCTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGCGCGGGGTGCCGCGCTGCCGCG
 CTGGCCCTCTCCCCAACCGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTCTCTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
 TTTACAACACTCTTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCACACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTGA
 AGAGCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGGCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCCTCCTCATGGCACTGCTGCCATCTTCTCCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTCTTCTTACTGGTGGCCCTGCTTCTTCCCATGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTCTGGCTGTGACTCTCCTGACTAGTGGCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAATGTGATTTTGGCCCTTGTGGCAGCACATCTCACACCCAAGAAG
 TTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAACCTGTGTCCATCAAAAAGACACTAAGGGATT
 TCCTCTGGGCTCAGTTCTATTTGTAAGATGGGAATAATCCTCTCTGTGAACCTCTTGTGA
 AAGATGATATGAGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCTGAAAGTGGTAAAGTGGGAACCACTGTGCTTTGAAACCAAA
 TTAGAAACACATTCCTTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTGTTTAAGGAGACCTCTTTTCAGTTTATCAAG
 TTATCATGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGACCTGGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWL RAGEERSGR PACQKANGFPDPKSSGSKKQK
QYQRIRKEKPQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNNTHA AVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSA AVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQV LALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGCTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCTCAGGCCCTTACGCTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCACT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACCTCCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAGACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52



FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGCCGGCAGAAAGGAGGCACCTTGAGAAATGTCTTTC
 CTCAGGACCCAAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTCAGGAGCCCTGGGGG
 TGCTGCCTTGGCATTGCTGCTTGCACACAGAGCTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTATGGGATGTATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATACCTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCCAAGG
 TGAGCAAGTCACCTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCAGTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAATGAGAAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

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MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKT'TGK
GIVKGRNLDNRGLILGAEAWGRGVKKNT

[illegible]

FIGURE 274

MGLFRGFVFLVLVLCCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCV
 LDKSGSMGGKDRNLNRMNQAAKHFLQLTVENGSWGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNATASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGYSYSLKVRAGH
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPRFEIDEDTQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIILTWTAPGDNFVGVKQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSINIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFIILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CCCTTAGGTGAAACCCGGGAGTAGAGTACTCAGCAAGAAGCGGGAAAGACCATACGTCGCCG
CGGAGGCGGAGGACAGCTGCTGCTGCTGATCTGCTGCTGGCTCGCTTCTTATCTCAAGAAAG
AGCCAGAGGATATTTCCACCGAGGAGCAATGATGTAGCCACCTCTTCAACCTTCCCTTCTTAACCT
CCCACTTATGCGAGATCTATAGAGATGTCACCTACCAACAGCAAGCGGCTCTTCGCGTATTAACCT
TGCGTTTGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGTGCAAGATGACTTCCCTTGA
GGGTGGACAGAGAAAGAAAGGACCTCCCTCTGCTGTGCTGCATACAGGAAGGCTGTGATGGG
AATGAAGGCTGAAATCTTGGAGATTTCACTTCAGTCATGCTTCTGCGTGCAGATACCTTTTAAAA
GTGAGAAAGCTTGCTCTGTGTGGTGTAACTCCAAAGAGCAGAACTGCTGTATAGAGAAATGGATG
CAAGCAGCTCCGGGGGGCCCAACCGCATGCTTCTGTGCTGTAGCCAGGAGAGCCCTTCGCTGGGG
GCCCGCGCTTTAGGGATGACCCGCGTTCTGGACGATGGCTGATCTTCAATGATGATGTTTCGG
GGGGGCTGTTTGGCTGATTTTCCGGGTGGTGGTTTGTGCTGGTGTGCTCTGCTGTGATCTCTG
CTCTGATAGTTTCCGCTGCACCCCAAAGGTCAGGAGAGGAGCGTGGCACTGCCAGGCGCAACGC
CCACCGGGGAAGGGGGATCCACGGCGCTCTCCAGGATGGGGAGAGCAGCCACACTGACCTTGA
GCAGCCTGAAGCGGCGAGATCGCACGCTCAAGGAGAGCTCGAGAGAGAGTGTAGCAGCTCAGAA
TGGGCACTACCAAGCCGCGAGTGTGCTGCTGGCTGGCTGTGCTGAGAGAGCTGAGAGAGAG
GCCGACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAG
CTTACCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAATCAGCCCTTGGAGAGCTGAACAATCTCGCAGAGAAGCCGCCAATACGCTCTTACAGCCCT
CTGATTTTCATAGAAGGATCTTCCAGCAACAGAAAGGACAAAGGACATTTGATAGACTCACTTCAA
AGGGGACCAAAACGAATTCAAACGCGCTATCTTATTCAGCACTTACGCCCATCATGAAGTGT
AAAAATGAAAGACTCAACATCGCGCAACACGCTTATCAATGTTATCGTGCTTCAACAAAAGGGTGG
ACAAGTTCCGCGCATCTATGCAAAATCTGGGAGATGTGCATGAGCAGGATGGGAGAGTCCATCT
CACTGTTGTTTACTTTGGGAAAGAAATAATAAGTCAAGGAAGTATTTGAAAACACTTCCAAA
GCTGCCAATCTGAGCAATTTTACCTTCTCATCGCTGAATGTGAGAATTTCTCGGGGAAAGGAGT
ATGTTGGAAGCCCGCTTGGAAAGGGAAGCAACGCTCTTCTCTTTTCTGTGATGTGCACATCTACT
CACATCTGAATTTCTCAATACGTTGTAGGCTGAATCAGCCAGGAGGAAGAGTTTATTCAGTT
CTTTTCAGTCAGTCAACTCTCGGATAATATACGGCCTTATATGATGACCTGATGATGATGATGAT
GCTGCTCATGAAGAGAAATGAG
GAG
CTTTATGCGAAGTATCTCCACAGCAACCTCATGCTGCTTACGAGCGCTTCGGGAGACTTCTCCAC
TTGCGATAGAAGCGCTGCATGCGACGACTGCCCCGAGCAGTACAAGATGTGATCAGTGTCAA
GGCCATGAACGAGGCACTCCACGGCCAGCTGGGATGCTGTGTTTCAGGCACAGATAGAGGTCAC
TCTCGCAACAGAAACAGAGACAGTACGAAAAAACAAGTCAAGACTCCAGACAGAGATTTGTGGAG
CACATTTTCTTCTTTGTGCAATTTGAGTCAAGAGTGCGCTCAACAGAGAAAAGACTTCCATTAAGAGC
ACAAAAGAAATGGACATGAGTGTGAGATGAGAAAGCTCGAATTTCTCTGTGTGGCTTTTAC
AAGCAAGATCAAATCTCCGCTTTGCTTCGAAAGATGACCCAGTTGCAACCTGTGAAGTGTCTGACA
AAGCAGAAATGTTGTAGATTTAAGAGCTAAATGTTGTGGAGTTTGTAGTGTGTTTACAACTACACT
GAGACCTGTGTTTGTGTGCTGATTAAGAAATTCATGATTTAAGCAGTTTGTAAAAAATCTCA
TAGATGAAGGCGAAGCATTTCTCTCATATGAATGAGCCTATGACAGGTTGAGAGAGGAGAGAG
AATGCTTAAATATCAGAGCGAGGAG
AG
AAAAATATCTGCTTATCTTTTGGTGTCTTTTAACTGCTCCGTTTTCCTTTTATTAAAAAT
GCACATTTTCCCTTGTGATATAGTCTGTAATTAATTAACCTTTCGAAGCTTCAAGAGA
CCCAAGTTGGCCTACATTTTATATTTTAAAGAAATACTTGGATGTCATTTAGCAACTTCA
GTTCAAGCATCAAAATGTATGTCATATCCAGGACATGCCAAATGCTGATTTGTCAGGCATGAAT
TCAGGACTTGAACATAGGAGAAAGTATTTGTACTAATACAGACGTACAGATGATTTTCTCGAA
GAGTATTTGGAAGGAGACATGAACACTGGAGAAAGAAATGACACTTCTGCTTACAGAA
AAGAAACTCATCAGACTGTGTATCTGATGTACTTAAAGCTCAGAAACCAATTTTCTCTCA
GAAGTAGGGACCGGCTCTTACCTGTTTAAATAAACCAATGATACCGTTGGAACCAACAACTATCT
TTTCAAAACAGGCTGCTCTCTCGGTTCTGGCTTCCATAGAAAGAAATGGAGAAAAATATATAT
ATATATATATATGTGAAAGATCATTCATCTGCGGAGATCTAGTGGATGAGAGTTTGTGTCATCA
GTATATCCCAACGAGCGAGGTGAAGATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAG
CAAGTGTGCTGAGGAG
CACTTAGTGCTTTTCACTTCATGTAATTTTAACTATTTTAAAAATTAATACAGTTA
CACTTAGTGCTTTTCACTTCATGTAATTTTAACTATTTAGCCAGCAGATGATGAGCTAATTTATCT
CTTGTGCTGTTCTGTTCTGTTTGTCTACAGCTAACTCACTTTTAAAGAGTTCAAGAAGCTTCAAGC
TCTTGGTGCTTTAAAAAATGCATTTGATTTGTTGATCTGTTGATTTGATTTGATTTGATTTGATTTG
AGGCCATGAATGGGAGGTGGTATGTCAGCACTAATAAATATGATTTGTGGATGATGA

FIGURE 276

MMMVRRGLLAWISRVVVLVLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPPEKPVVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKCMQMS
KAMNEASHGQIGMLVFRHEIEAHLRKQKTSSKKT

FIGURE 277

GAAAGAAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACCAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCTGCTTCTCAAGAAATTAACATTTGTTTCTGTGTACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGAATAAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGATAAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTtagaaataagatcaggcatatgtatatatTTTTCACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTGGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATTTTTCTGAATATCAGCCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKC
ENMITTIENGIPSDPLDMKGGILMMP

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FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAAGCTGGGTTTCCCT**CATGT**
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCCGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAAGACCGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTCGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGACAA
 GAACCCTAGTATTTCTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCACTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCACTCATACACAGCCTCATTATTAAGGTCTTATTTAATTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGCTCTGTACATTTCTTTCAGTATTTCTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCCCTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAAGTAAATCCTAAATTCAAACGTGTTAAATGACATTTTATTTTTATGTCTC
 TCCTTAACATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDFFQPMsGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVDGVIGIIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCTGTGATTTT
ATCCAACTACTTACCTTGCTACGATATCCCCTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAA

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTCTGGGTACGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGCCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCACTAAACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAACCTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
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FIGURE 285

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAAGTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
 GACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAAGTCTCTGGGGCAGGAGGTGAGC
 CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCACGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAACTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAAGTGGAG
 GACCAATCATGCTGCAAGGAACACTTCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACCTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTEILGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTCCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGTTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCTGTGCGCAGCAGCAAGAGATACATATCGAGTTCACCATCCC
 TAA**ATAGT**CTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCCTTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATTTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATGATCCATGTGCACGCAGATAAAATGGCTTCTGTCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTAACAAACCCAGTTTGTCTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTGTCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCCTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGCTCT
 GCCATATCAGAACACAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTCATTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT
 CAAAGAAGCAGATGTCATGATAAACGGAATAGAAAAAAGAACCTACATTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTACATTT
 TCGTATATTTATTTTTTTAGCCATCATATATGTTTAAGTCTATTATGGGCAACCAATCTT
 TGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAAATGCATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTGTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGAATTAAGTTTGTGCTGTTTTCATGTCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRVRDKDGDCLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGCTTCAGCCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 290

MKLAALLGLCVALSCESSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLLS
SLGIPVNHIEGSQKCVAELGPQAVGAVKALKALLGALTVFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACC GGCTTGGCCCCAGTCTCTCAGTCGCCAGAGACCCCAGCCCC
 TCAGAACCCAGACAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAAGGCCGGTGAGGAAGAGAAAAGCCTGGCTGATGGCCAGCAGGCGAGCAGCTT
 GCCAAGGAGACTTCAAACCTCCGATTACGCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAAACCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
 CCGGGCTCTGCTCTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCCCAACCTGGAAGT
 GGGCTCTCACAGGGGAGTTTTCCTTATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTTCCCAAAC
 GTTGATGAGATTAATCCTGAAACCAAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTGCAGACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTGTGCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGAGAAAATGGGTGACCACCTCGCCCTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAAACATGAAACCCAGAAACATGGAAGTTTCTTTCCGAAGTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAAATCTTCTACCCCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTATCGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAATTAAC
 TGCTTATTCATGCCTCCTGTCAACAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTCTGCGGCAGGGTGGTGAATCCGACTCTCCTATTAATTGAGG
 ACATGCATAAGCACTTCTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTCTTTGTTCTTAAGTATTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCACCTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTCTTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGCAGGGGAGAAATTC
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCCTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTAAATGTTTTTGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAATTTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCTATCAAGATGCAAGTCAAACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCACTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 295

AGAAAGCTGCACTCTGTGTAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCATTGTATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCTTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGCACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCGAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
 TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTGTATTGGAGTGATATGGAACCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
 GGAGGGAAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVFNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYS PYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEAS PQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAAATGGGACTCGGCGCGGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTGTGTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATGTATGCTGCCCTATCAATTAATTTGGTTTATTAATAGTTAAACCAATATCTCT
 CTTTTTGAATAAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAAAGTCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAI I

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGCATGGCGACCCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGCGCTTTCGCTGCTGCTGCTGGC
 GCAGCTGTGAGACGCGCCGAAGAATTTGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCACGCTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAAGTACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGTGATTTACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAAGTGTGCTGATTTTTTTTTCTGTGTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTG
 TTGTTGTTGTTTTTGTGTTGTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGT
 AACAACCTTTTCAAGTCACTTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACCTGACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCTGGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTTGGGTGCCTCTTCTGAAAGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTTGGAATGTAAACAATAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLSCLALSVELLAQLSDAAKNFEDVRCKCICPPYKENS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIYLSILGLLLLYM
VYLTLEPILKRRLFQHAQLIQSDDDIGDHQPFANAHDVLAARSRSRANVLNKVEYA
QQRWKLQVQEQ
RKSVFDRHVVL

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGATGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTA AAACTTCTTATAGTTTATAAAATTATTTCAAATCCATCATCTCTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTACATAAGAATG
TTTACTCAATGTTTAAAGTGTTTTGCCCAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGAGGGGSGRGLMGQIIPYGFGIPLYILYILFKVSRIILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCACTGAAACTCATCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTACAGTCTGTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCTTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATCTTATGCT
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTACAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTAAACACGTGACCAAGGTAGAATGGATATTTTCCAGGACGCGCGCAAAGGA
 GGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCT
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACTACATGACCATGCA
 CCCAGTTTGCCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTTGGGCCACTCTACCAGTGATTTTCCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAACCCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYNSLSPVIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRLMSVEYSQSWGHEFQNRVNLVGDIFRNDGSIMLQGVRES DG GNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHEFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKS GGGMPKTQQAF

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FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACTACATTTTGCAAAGTCATTGAACCTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCTGACTCCGACCCAGGCAGCCAGCAGCCCGCGGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGTGTAAGCCCGAGTCCGGAGAA
GCCCCGGGCAAACGCAAGGCTAAGGAGACCAAGCGGCGAAGTCCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAGTTCAAATTTGTGAGTACATTACCAAACAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDNKLNVSFVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIQVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACGTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGCGAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCGAG
 CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGGCGCTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGGAGCCGGCCGGTGTGCG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCCCGCGCGCCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACGTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCC
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTAAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTGTCTTGGCCGGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATAACAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAA CAGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGTCCTCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
 RQDPQLKGIVTRLYCRQGYLLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCGCTTGCAAAAAAT
 GAAGGATGACGAGACGACGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AATAAACACGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGCACATAAATAAATAATCTTAAAGCAGCTGTCCCG
 CTCGCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCATT
 TTCTCTATAAAGGAGAAAGTGAGCCAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAAACAGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAAATGACGGATAATGCAAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACACCTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGCCAACACAGATAAATATGATG**ATG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGCTTAGTTTAAACAGGCGCTATTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTCTTGTGGTGGCTGGTGTGGTGGCGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACGATTCAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACAGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCATTGAG
 GCATTGAAAATCCTACAGTTGAGTAGGAACCATATCAGAACCAATGAAATTTGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCGGAATGGAGCTTTTGATATCTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT
 GCGCGGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGAAGTGCCCTTGAAGGCTGTGCAACT
 TGAGGTATTTGAACCTTGCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCAATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAATTAACATTACTGCCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGGAACGTGTAACGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCGTCGACACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAATGGAACAGTCAAGACACA
 TGGGGCGTACAAAGTCGCGATAGCTGTGCTCAGTATGGTACGTTAAATTTCACAAAATGTAAGTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATTCGGTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCGAG
 GACCACAGATAACAATGTGGGTCACCTCCAGTGGTGCAGTGGGAGACCAACATGTACCACCTCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTCAACATCCAGTGACTGATATAAAGAGTGGGATCCCGGAATT
 GATGAGGTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGGCCACTGCGCATGCCTGTCTCAGAGATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCTTCAACACACACAACAGTTAAACACAATAAATTCATACACA
 CAGTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTTAAGACAATGTACAAGAGACTCAATCT**TA**AAACA
 TTTACAGAGTTCAAAAAACAACAATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTTAA
 ATCTACTGTTTCAAAAAGTGCTTTACAAAAAACAACAAAGAAAGAAATTTATTTATTAATAAATCTATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRVYLNLAAMCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMLHQLK
 WMIQSQIQVIERNAFDNLSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCIDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVQDTGMYTCMVSNSVGN
 TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGFTPVVDWETTNVITSLTPQ
 STRSTKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHNTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCGGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCCGAGGCGCGCGCCAGCTCGCCGAGGTCGGTCGGA
 GGGCCCGGGCCGCCCCGAGGCCAAGCAGCACTGAGCGGGGAAGCGCCCGGTCGGGGGATC
 GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGTGCTCACCAGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGAGAGGATGAACGTCTGCCCTCCCAAAATCTAGGATT
 GACTACAACCACCTGGACGAGTTCTGCTGCAGAAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAACCTGTACAGT
 ATGTACAAGACATCGGCATGGTTGCAGGAGCAGTGACAGGCTAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGGCCGCTCTTGTGAACCCAGCT
 CCTCTTCTCAGGCTCTGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGT**TGA**ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCGCCACACAACAGATGAGAGGTCTCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTGATGAGCATTTCCTTATACAATACCAAAACAGCAAA
 AGGATGTAAGCTGATTCATCTGTA AAAAGGCATCTTATTGTGCCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACTTTTAAATGTGGGATATTTGTATCAGTGCTTTGATTACAAAT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTGACAGCTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTCTTCTATTCTGACTTAAC
 TTCAATTTGTCTATAAGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATTAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCTATGTTT
 ATGAGGATTGTTGACAAACATAGAAATATATAATGGAGCAATTTGTGGATTTCCTTCAAAT
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACAACATGTCATT
 TATCAACGCTTGTAGAAGAAATCTTCTAGAGAAAAGGATAGAAATGCTGAAAGATTA
 CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAATGTGAACACAGAATGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGAAAATCCAGCAGGTGGAGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQFGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

[illegible]

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLLCFVLLCGVVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHVLVVKPSGARCYPVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQDQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTFPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCGTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTCAGCATCACTTACAGGACCAGAGGGACAAACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAAGCCTGTGGACTTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGTGCTGGCGACAGCCTCTCAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCTGT
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCGAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTATTCTCTACTCTGGCCAACAACCT
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAAGCCCTTGGGGAAAGTGGACATTCTTCTGACCTGGATGCGAAAATTCTACAAGC
 TCTCAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTCCCTGTGTCATTTCA
 AACAGTCTCCCTTCCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAG
 CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAACTCCTTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTCCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARFFCPPLLATASQMVMVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CAGTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACCGGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
 GGTCTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACG**ATG**TTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCTAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAAGTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTCAACACC
 CCCATACCACGGCGGCACCCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCCGATGACCCCGGCCCGGCCCTCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCAGTGAAC
 ACGCAGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGGCTCTGCCCTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGAGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGCACCGA
 TGACAGCTCTGAAGAGGCAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAAATTGCAGCATCAGAAAATAGAAACAACACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTCCCCACCAGCAGGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TGAG**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAATCCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
 TTAATAATTCACCTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTTITGSDPEEAI FDTLCTDDSSSEAKILTM DILT LAHTSTEAKGLSSESSASSD
 GPHPVITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTLLAEALVT
 VTNIEVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVT
 TASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETS
 SALS VETPSYVKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFPTSETPTMDI
 ATKGFPTSRDPLPSVPPTTTNSSRGNTSLAKITTSAKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGGATTGCGCGGTCTTCCGCGGG
 GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGAGGCCA
 GAGAGAAATCTCATCTGTGCGAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAACACGCA
 AAAGGACTTATGAGTTACAGGATAAATACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATCTCTCTTACATGGCCAATTTTCAACAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACCTTCTC
 AGCCTCCCACGACCTCATTTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTTCTGACTACCACCTTTTCAAGCACCTACGAGCTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCATTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGCTCTTAAATTCATT
 TAGTAACCAAGACCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTCGGGTGATTTTTGTATTTTGTAGTAGAGACGGGGTTTCCACATGTTGGTCAGGCTG
 GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCTCCCAAAGTGTCTGGGATTACAGG
 CATGAGCCACCACAGCTGCCCCCTTCTGTTTTATGTTTGGTTTTGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAAATTGCCATATAAAATTTCAAATTCACCTGGCTTTTATGCAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGAATTCCTTTAAACCTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTINTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCACGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTGGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGACACTGTGT
 CCGTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTCTGCTGGCACCATTCTATGCAGAAGAAGGCGAGGAGACAA
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGACAGCCCAAGGCAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGCGAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTGCGAGGGACTTCCAGTACGGGACGAAAGGACTTCTCAGTACAC
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 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA
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 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGCGGACCCTGCCTTCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCTAAACATGCCAGTGACTGTCGCACTTGAGTTTGAGGGCCAGTGGGCGTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCTTGGTCAGGTCAAGTGCACTTGCCAGGATAAGCCAGGACCGGCACAGAAGTGG
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 TTTACAGAGCAATTACTTGTATATACAACTTTGTATCTGCCTTTTCCACCTTATCGTTCC
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FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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FPGPCCPPSPSPFTQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEEAPPLPG
TSQYGHERTSQYTGTSHPHATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIIPMRI
LAPVLVLLSLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAAEKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128